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OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 13:36:38 ; Search time 696 Seconds
(without alignments)

10827.343 Million cell updates/sec

Title: US-10-018-392A-3

Perfect score: 1273

Sequence: 1 ggctctcactaactaatca.....atcctctatcttgaatctt 1273

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: N_Geneseq_16Dec04:*
2: Geneseqn1980s:*
3: Geneseqn1990s:*
4: Geneseqn2000s:*
5: Geneseqn2001as:*
6: Geneseqn2001bs:*
7: Geneseqn2002as:*
8: Geneseqn2002bs:*
9: Geneseqn2003as:*
10: Geneseqn2003bs:*
11: Geneseqn2003cs:*
12: Geneseqn2003ds:*
13: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1273	100.0	1273	4	Aaf54017
2	1273	100.0	1707	6	Aai171008
3	1273	100.0	2775	3	Aaa54034
4	1273	100.0	2804	8	Abv77053
5	1273	100.0	38059	4	Aaf54018
6	1273	100.0	38059	6	Abn95627
7	1273	100.0	38059	10	Add71098
8	1272	99.9	1272	4	Aaf54080
9	1271.4	99.9	1273	4	Aaf54074
10	1271.4	99.9	1273	4	Aaf54073
11	1269.8	99.7	1273	4	Aaf54075
12	1269.8	99.7	2792	2	Aax28626
13	1268.2	99.6	2781	1	Aan40142
14	1268.2	99.6	2802	2	Aat02460
15	1266.6	99.5	1273	4	Aaf54076
16	1261.8	99.1	2781	1	Aan40177
17	1261	99.1	1272	4	Aaf54079
18	1261	99.1	1275	4	Aaf54077
19	1260	99.0	1276	4	Aaf54078
20	1258.6	98.9	2728	13	Adq38340

21	1258.6	98.9	2771	13	Adq38338
22	1258.6	98.9	2777	13	Adq38339
23	1258.6	98.9	2831	13	Adq38341
24	1257.4	98.8	2758	13	Acn43105
25	1257.4	98.8	2766	13	Acn43104
26	1174.6	92.3	2807	1	Aan60543
27	1174.6	92.3	2807	12	Adh42198
28	883.4	69.4	1971	4	Abas5251
29	883.4	69.4	1971	4	Abas28575
30	200.6	15.8	201	13	Adq40547
31	200.6	15.8	201	13	Adq40266
32	200.6	15.8	201	13	Adq40829
33	200.6	15.8	201	13	Adq41116
34	186	14.6	1438	6	Abq82328
35	186	14.6	1438	12	Adh42196
36	186	14.6	1638	1	Aan50351
37	186	14.6	1639	1	Aan50049
38	186	14.6	1639	1	Aan50362
39	157	12.3	1612	12	Adh42200
40	154	12.1	154	4	Aaf54087
41	153	12.0	153	4	Aaf54119
42	153	12.0	153	4	Aaf54088
43	152.6	12.0	422	8	Abx47596
44	152	11.9	152	4	Aaf54120
45	152	11.9	152	4	Aaf54089

ALIGNMENTS

RESULT 1

Aaf54017

ID AAF54017 standard; DNA; 1273 BP.

XX

AC AAF54017;

XX

DT 30-MAR-2001 (first entry)

XX

DE hFIX gene 3' UTR age-related regulatory region AE3', SEQ ID NO:3.

XX

KW Age-related gene regulation; gene expression; human factor IX; hFIX;

KW AE3'; 3' UTR; 3' untranslated region; AE3'; element;

KW age-regulatable expression construct; antisense therapy; gene therapy;

KW thrombosis; cardiovascular disease; diabetes; Alzheimer's disease;

KW Parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia; ds.

XX Homo sapiens.

OS

XX WO200075279-A2.

XX

XX 14-DEC-2000.

XX

XX 06-JUN-2000; 2000WO-US015728.

XX

XX 09-JUN-1999; 99US-00328925.

XX

XX (UNMI) UNIV MICHIGAN.

XX

XX Kurachi K, Kurachi S;

XX

XX WPI; 2001-061708/07.

XX

XX New regulatory elements that control age-related gene expression, useful

XX in gene therapy and for reducing factor IX expression.

XX

XX Claim 1; Fig 3A; 225pp; English.

XX

XX The invention relates to nucleic acid sequences which regulate gene expression in an age-related manner and/or in a liver-specific manner.

XX The invention identifies regions of the human factor IX (hFIX) gene, and

XX a region of the human protein C (hPC) gene, which are age-related

XX regulatory sequences. The hFIX age-related regulatory sequences are

XX designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'

UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34383-35655 of AAF54018) respectively. These elements act synergistically to increase hFIX levels over the lifespan of an individual; however, they can independently exert effects on hFIX mRNA in an age-related manner, with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX mRNA levels, over time. AE5' also directs liver-specific expression. The hPC gene age-related regulatory sequence is found in the 5' UTR (AACGAGAA-3', and contains two PEA-3 (polyoma virus activator 3) elements 5'-GAGGAAA-3' and 5'-CAGGAAAG-3'. The age-related regulatory sequences of the invention, along with their homologues, variants and fragments, may be used in the construction of recombinant expression vectors for the expression of a desired sequence in an age-related fashion in a host cell. Preferred target genes for expression in such age-regulatable expression vectors include those encoding proteins involved in blood coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the anti-coagulants protein C and antithrombin III), human alpha-1-antitrypsin, PEA-3 protein and reporter proteins such as luciferase. Preferred promoters for use in such age-regulatable expression vectors include the human factor IX promoter, the T7 promoter, the T3 promoter and the SP6 promoter. The expression vectors of the invention may be used in gene therapy to provide age-related and/or liver-specific expression of target genes. Age-regulatable constructs may be used in the treatment of such age-related conditions such as thrombosis, cardiovascular disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer, osteoporosis, osteoarthritis and dementia. Specifically, they may be used to express factor IX antisense mRNA in the treatment of thrombotic conditions associated with the natural age-related rise in factor IX expression. Transgenic cells or animals that contain vectors of the invention are useful as models of these diseases, in screening for potential therapeutic agents and for studying normal processes such as ageing and gene expression. Fragments and homologues of age-related regulatory sequences, are useful as probes to detect, isolate or identify other such sequences in samples. The present sequence represents the hFIX 3' UTR (untranslated region) age-related regulatory sequence ARI',

Sequence 1273 BP; 392 A; 263 C; 217 G; 401 T; 0 U; 0 Other; 22 X

Query Match	100.0%;	Score 1273;	DB 4;	Length 1273;
Best Local Similarity	100.0%;	Pred. Nl. 6.7e-279;		
Matches 1273; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GGCCTCTCACATAACTACCTTTCCCATCTTTTCTTAGATTGAAATATATACATTCAT	60	
Db	1	GGCCTCTCACATAACTACCTTTCCCATCTTTTCTTAGATTGAAATATATACATTCAT	60	
Qy	61	GATCATTTGCTTTTCTCTTTTACAGGGGAAATTTTCATATTTTATCTGAGCAAAATGATTA	120	
Db	61	GATCATTTGCTTTTCTCTTTTACAGGGGAAATTTTCATATTTTATCTGAGCAAAATGATTA	120	
Qy	121	GAAATGGAAACCACTAGAGGAAATATAATGTGTAGGAAATACAGTCAATTTCTAAGGGCC	180	
Db	121	GAAATGGAAACCACTAGAGGAAATATAATGTGTAGGAAATACAGTCAATTTCTAAGGGCC	180	
Qy	181	CAGCCCTTGACAAATTTGTGAAGTTAAATTTCCACTCTGTCCATCAGATACTATGGTTC	240	
Db	181	CAGCCCTTGACAAATTTGTGAAGTTAAATTTCCACTCTGTCCATCAGATACTATGGTTC	240	
Qy	241	TCCACTATGGCAACTAATCTCAATTTTCCCTCTTAGCAGCAATCCATCTTCCCGAT	300	
Db	241	TCCACTATGGCAACTAATCTCAATTTTCCCTCTTAGCAGCAATCCATCTTCCCGAT	300	
Qy	301	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	360	
Db	301	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	360	
Qy	361	TTTGGTCTACTCTATCAAGGCCAGTACCACTCATGAGAAAGACACAGGAGTAGC	420	
Db	361	TTTGGTCTACTCTATCAAGGCCAGTACCACTCATGAGAAAGACACAGGAGTAGC	420	
Qy	421	TGAGAGGCTAAAACTCATCAAAAAACACTACTCCTTTTCTCTACCTTATTCCTCAATCTT	480	
Db	421	TGAGAGGCTAAAACTCATCAAAAAACACTACTCCTTTTCTCTACCTTATTCCTCAATCTT	480	

XX PD 27-DEC-2001.
 XX PF 19-JUN-2001; 2001WO-US019634.
 XX PR 20-JUN-2000; 2000US-0212902P.
 XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX PA (UNIW) UNIV WASHINGTON.
 XX MIao CH, Kay MA;
 XX WPI; 2002-114582/15.
 XX Nucleic acid construct for expressing nucleic acid molecules, proteins in
 PT mammalian liver cells, has operably linked hepatic locus control element,
 PT hepatic promoter, coding sequence, polyadenylation signal and intron.
 XX
 PS Example 1; Page 57-59; 64pp; English.
 XX
 CC The present sequence is that of the 3' untranslated region (3' UTR) of
 CC the human Factor IX gene. The 3' UTR, which includes a polyadenylation
 CC signal. It was incorporated into expression cassettes of the invention
 CC that were designed for liver-specific expression of Factor IX. The
 CC cassettes also include an hepatic locus control element, an hepatic
 CC promoter located 3' to the hepatic locus control element, a Factor IX
 CC coding sequence, and an intron (see AAI71003-16). Also provided are
 CC vectors that include an expression cassette of the invention. These may
 CC be episomal or integrating vectors, including viral vectors, and are used in
 CC a claimed method of ameliorating disease. A therapeutic amount blood
 CC clotting Factor IX is produced in mammalian liver cells for at least 100
 CC days, and preferably at least 500 days. In examples of the invention,
 CC human Factor IX was expressed in mouse liver cells following injection of
 CC retrovirus-based plasmids that carried the expression cassettes into the
 CC tail vein or portal vein, and by direct injection of plasmid DNA into the
 CC liver
 XX
 SQ Sequence 1707 BP; 500 A; 362 C; 305 G; 540 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1273; DB 6; Length 1707;
 Best Local Similarity 100.0%; Pred. No. 7.2e-279;
 Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GGCTCTCTCACTAATCACTTTCCCATCTTTTGGTAGATTTGAATATATACATTTCTAT 60
 51 GGCCTCTCACTAATCACTTTCCCATCTTTTGGTAGATTTGAATATATACATTTCTAT 110
 61 GATCATGTCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAATTTGATTA 120
 111 GATCATGTCTTTTCTTTTACAGGGGAGAAATTCATATTTTACCTGAGCAATTTGATTA 170
 121 GAAATGGAAACCACTAGAGGAATATATGTTGTTAGGAATTTACAGTCATTTCTAAGGGCC 180
 171 GAAATGGAAACCACTAGAGGAATATATGTTGTTAGGAATTTACAGTCATTTCTAAGGGCC 230
 181 CAGCCCTTGACAAAATTTGTAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 240
 231 CAGCCCTTGACAAAATTTGTAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 290
 241 TCCACTATGCACTAATCACTCAATTTTCCCTCTTAGCAGCATTTCCATCTCCCGAT 300
 291 TCCACTATGCACTAATCACTCAATTTTCCCTCTTAGCAGCATTTCCATCTCCCGAT 350
 301 CTCTCTTGTCTTCTCCAAACCAATCAATGTTTATTTAGTTCTGTATACAGTACAGATC 360
 351 CTCTCTTGTCTTCTCCAAACCAATCAATGTTTATTTAGTTCTGTATACAGTACAGATC 410
 361 TTTGGTCTACTCTATCACAAGGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420
 411 TTTGGTCTACTCTATCACAAGGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
 421 TGAGAGGCTAAACTCATCAAAACCACTACTCTCTTCTCTACCCCTATTCCTCAATCTT 480

Db 471 TGAGAGGCTAAAACTCATCAAAACCACTACTCTCTTTTCTCTACCCCTATTCCTCAATCTT 530
 QY 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 540
 Db 531 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 590
 QY 541 TTTTACCCTCCATGTCGTGTTAAAGGAGAGATGGGAGCATCATCTCTGTTATATCTCTGTA 600
 Db 591 TTTTACCCTCCATGTCGTGTTAAAGGAGAGATGGGAGCATCATCTCTGTTATATCTCTGTA 650
 QY 601 CACAGTTATACATGTCATCAAAACCCAGACTTCTCTCCATAGTGGAGAGCTTCTTTTCAG 660
 Db 651 CACAGTTATACATGTCATCAAAACCCAGACTTCTCTCCATAGTGGAGAGCTTCTTTTCAG 710
 QY 661 AACATAGGAGATGAAGTAAAGTCTGCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
 Db 711 AACATAGGAGATGAAGTAAAGTCTGCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 770
 QY 721 AAGTTATTTTAG 780
 Db 771 AAGTTATTTTAG 830
 QY 781 TCTGTGTGTATGCTGT 840
 Db 831 TGT 890
 QY 841 AGCCATTTCTAAGAGCTTGT 900
 Db 891 AGCCATTTCTAAGAGCTTGT 950
 QY 901 AGATTGGCATATCATTTGTAACATAAAAGCTGACATTTGAGGAGTGTGTGTGTGTGTGTGTGTGT 960
 Db 951 AGATTGGCATATCATTTGTAACATAAAAGCTGACATTTGAGGAGTGTGTGTGTGTGTGTGTGTGT 1010
 QY 961 CTAAAAATAG 1020
 Db 1011 CTAAAAATAG 1070
 QY 1021 CTAGTAGAGACTTTGAGGAGAAATTTCAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
 Db 1071 CTAGTAGAGACTTTGAGGAGAAATTTCAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1130
 QY 1081 AAGAAGTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTCTTTAACTAGCATATA 1140
 Db 1131 AAGAAGTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTCTTTAACTAGCATATA 1190
 QY 1141 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGCATTAAGTCATTTCCCATCAGCCAACT 1200
 Db 1191 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGCATTAAGTCATTTCCCATCAGCCAACT 1250
 QY 1201 AAGTTGTCTCTTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 1260
 Db 1251 AAGTTGTCTCTTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 1310
 QY 1261 TATCTTGAATCTT 1273
 Db 1311 TATCTTGAATCTT 1323
 RESULT 3
 AAA54034
 ID AAA54034 standard; DNA; 2775 BP.
 XX
 AC AAA54034;
 XX
 DT 08-FEB-2001 (first entry)
 XX Human factor IX coding sequence.
 DE
 XX Vitamin K dependent protein; VKDP; gamma-carboxylation; chimeric protein;
 KW fusion protein; coagulation factor; Factor X; Factor VII; Protein S;
 KW Factor IX; Protein C; prothrombin; blood clotting; haemophilia; human;
 KW ds.

ID	ABV77053 standard; DNA; 2804 BP.
XX	
AC	ABV77053;
XX	
DT	03-MAR-2003 (first entry)
XX	
DE	Nucleotide sequence of human Factor IX.
XX	
KW	Factor VIII; non-viral vesicle vector; vesicular membrane; hepatitis B;
KW	envelope protein; factor IX; liver cell; gene therapy; haemophilia; gne;
KW	ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 30..1415
FT	/tag= a
FT	/product= "Factor IX"
XX	
PX	WO200286091-A2.
XX	
PD	31-OCT-2002.
XX	
PF	25-APR-2002; 2002WO-US013164.
XX	
PR	25-APR-2001; 2001US-0286314P.
XX	(REGC) UNIV CALIFORNIA.
PI	Chien KR, Hoshijima M;
DR	WPI; 2003-093125/OB.
XX	P-PSDB; ABB99529.
PT	New non-viral vesicle vector comprises vesicular membrane with hepatitis
PT	B envelope protein and nucleic acid expression construct comprising
PT	complete factor VIII or IX coding sequence, useful for treating
XX	hemophilia.
PS	Disclosure; Page 19-21; 34pp; English.
CC	The present sequence encodes a human Factor IX. Factor IX polynucleotides
CC	are used to construct non-viral vesicle vectors. These vectors comprise a
CC	vesicular membrane with hepatitis B envelope protein exposed on the
CC	vesicle surface, and a nucleic acid expression construct comprising a
CC	complete factor VIII or factor IX coding sequence and a promoter sequence
CC	functional in liver cells. The non-viral vesicle vector is useful in gene
XX	therapy protocols for treating haemophilia
SQ	Sequence 2804 BP; 868 A; 536 C; 568 G; 832 T; 0 U; 0 Other;
Query Match 100.0%; Score 1273; DB 8; Length 2804;	
Best Local Similarity 100.0%; Pred. No. 8.2e-279;	
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GGCGTCTCACTAACTAATCATCTTTCCCACATCTTTGGTAGATTGGAATATATACACTTCAT 60
Dd	1464 GGCGTCTCACTAACTAATCATCTTTCCCACATCTTTGGTAGATTGGAATATATACACTTCAT 1523
Qy	61 GATCATTGCTTTTCTCTTTACAGGGGAGAATTTGCATAATTTTTACCTGAGCAAATTTGATTA 120
Dd	1524 GATCATTGCTTTTCTCTTTACAGGGGAGAATTTGCATAATTTTTACCTGAGCAAATTTGATTA 1583
Qy	121 GAANAATGGAACCACTAGAGGAATATATGTGTAGGAATTTACAGTCATTTCTAAGGCC 180
Dd	1584 GAANAATGGAACCACTAGAGGAATATATGTGTAGGAATTTACAGTCATTTCTAAGGCC 1643
Qy	181 CAGCCCCITGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCAATCAGACTATGTGTC 240
Dd	1644 CAGCCCCITGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCAATCAGACTATGTGTC 1703
Qy	241 TCACACTATGGAACTAACTCACTCAATTTTCCCTCCTTTAGCAGCATTTCCATCTTCCGAT 300

ID AAF54018 standard; DNA; 38059 BP.
AC AAF54018;
XX
XX 30-MAR-2001 (first entry)
XX Human factor IX (hFIX) gene, SEQ ID NO:4.
XX
XX Age-related gene regulation; liver-specific; gene expression;
KW human factor IX; hFIX; AE3'; age-regulatable expression construct;
KW antisense therapy; gene therapy; thrombosis; cardiovascular disease;
KW diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;
KW osteoarthritis; dementia; ds.
XX Homo sapiens.
XX
XX WO200075279-A2.
PN
XX 14-DEC-2000.
XX
XX 06-JUN-2000; 2000WO-US015728.
PF
XX
XX 09-JUN-1999; 99US-00328925.
PR
XX (UNMI) UNIV MICHIGAN.
XX
XX Kurachi K, Kurachi S;
PI
XX
XX WPI; 2001-061708/07.
DR P-PSDB; AAB60281, AAB60282, AAB60283, AAB60284, AAB60285, AAB60286,
DR AAB60287, AAB60288, AAB60289.
XX
XX New regulatory elements that control age-related gene expression, useful
PT in gene therapy and for reducing Factor IX expression.
XX
XX Disclosure; Fig 8A-E; 225pp; English.
PS
XX The invention relates to nucleic acid sequences which regulate gene
CC expression in an age-related manner and/or in a liver-specific manner.
CC The invention identifies regions of the human factor IX (hFIX) gene, and
CC a region of the human protein C (hPC) gene, which are age-related
CC regulatory sequences. The hFIX age-related regulatory sequences are
CC designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'
CC UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34393-
CC 35655 of AAF54018) respectively. These elements act synergistically to
CC increase hFIX levels over the lifespan of an individual; however, they
CC can independently exert effects on hFIX mRNA in an age-related manner,
CC with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX
CC mRNA levels, over time. AE5' also directs liver-specific expression. The
CC hPC gene age-related regulatory sequence is found in the 5' UTR
CC (AAF54081), and contains two PEA-3 (polyoma virus activator 3) elements
CC (AAF54081-3' and 5'-CAGGAAG-3'). The age-related regulatory sequences of
CC the invention, along with their homologues, variants and fragments, may
CC be used in the construction of recombinant expression vectors for the
CC expression of a desired sequence in an age-related fashion in a host
CC cell. Preferred target genes for expression in such age-regulatable
CC expression vectors include those encoding proteins involved in blood
CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
CC anti-coagulants protein C and antithrombin III), human alpha-1-
CC antitrypsin, PEA-3 protein and reporter proteins such as luciferase.
CC Preferred promoters for use in such age-regulatable expression vectors
CC include the human factor IX promoter, the T7 promoter, the T3 promoter
CC and the SP6 promoter. The expression vectors of the invention may be used
CC in gene therapy to provide age- related and/or liver-specific expression
CC of target genes. Age-regulatable constructs may be used in the treatment
CC of such age-related conditions such as thrombosis, cardiovascular
CC disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,
CC osteoporosis, osteoarthritis and dementia. Specifically, they may be used
CC to express factor IX antisense mRNA in the treatment of thrombotic
CC conditions associated with the natural age-related rise in factor IX
CC expression. Transgenic cells or animals that contain vectors of the
CC invention are useful as models of these diseases, in screening for
CC potential therapeutic agents and for studying normal processes such as

CC	ageing and gene expression. Fragments and homologues of age-related	
CC	regulatory sequences, are useful as probes to detect, isolate or identify	
CC	other such sequences in samples. The present sequence represents the hFIX	
CC	gene	
XX		
SQ	Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 1273; DB 4; Length 38059;	
	Best Local Similarity 100.0%; Pred. No. 1.6e-278;	
	Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GGCCTCTCACAACCTAACTACCTTTCCCATCTTTTGTAGATTGTAATATATACATTTCTAT 60	
DB		
DB	34383 GGCCTCTCACAACCTAACTACCTTTCCCATCTTTTGTAGATTGTAATATATACATTTCTAT 34442	
QY	61 GATCATTCCTTTTCTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTA 120	
DB		
DB	34443 GATCATTCCTTTTCTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTA 34502	
QY	121 GAAATGGAACCACTAGAGGAATATAATGCTGTAGGAAATTTACAGTCAATTTCTAAGGGCC 180	
DB		
DB	34503 GAAATGGAACCACTAGAGGAATATAATGCTGTAGGAAATTTACAGTCAATTTCTAAGGGCC 34562	
QY	181 CAGCCCTTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC 240	
DB		
DB	34563 CAGCCCTTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC 34622	
QY	241 TCCACTATGGCAACTAATCACTCAATTTTCCCTCTTTAGCAGCAATTCATCTTCCCGAT 300	
DB		
DB	34623 TCCACTATGGCAACTAATCACTCAATTTTCCCTCTTTAGCAGCAATTCATCTTCCCGAT 34682	
QY	301 CTTCTTTTCTCTCCCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360	
DB		
DB	34683 CTTCTTTTCTCTCCCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 34742	
QY	361 TTTGCTCTACTCTATCAACAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGGATGAGC 420	
DB		
DB	34743 TTTGCTCTACTCTATCAACAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGGATGAGC 34802	
QY	421 TGAGAGGCTAAACCTATCAAAAACATCTCTCTTTTCCCTCTACCCCTATTCCTCAATCTT 480	
DB		
DB	34803 TGAGAGGCTAAACCTATCAAAAACATCTCTCTTTTCCCTCTACCCCTATTCCTCAATCTT 34862	
QY	481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 540	
DB		
DB	34863 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 34922	
QY	541 TTTTACCCCTCCATGGTCCGTTAAAGGAGAGATGGGGAGCATCATCTGTTATACCTTCTGTA 600	
DB		
DB	34923 TTTTACCCCTCCATGGTCCGTTAAAGGAGAGATGGGGAGCATCATCTGTTATACCTTCTGTA 34982	
QY	601 CACAGTTATACATGCTTATCAAAACCCAGACTTGTCTTCCATAGTGAGAGACTTGTCTTTTCAG 660	
DB		
DB	34983 CACAGTTATACATGCTTATCAAAACCCAGACTTGTCTTCCATAGTGAGAGACTTGTCTTTTCAG 35042	
QY	661 AACATAGGATGAAGTAGGTCCTGAAAGCTTTGGGGGAAAGCTTTCTTTCAGAGAGTT 720	
DB		
DB	35043 AACATAGGATGAAGTAGGTCCTGAAAGCTTTGGGGGAAAGCTTTCTTTCAGAGAGTT 35102	
QY	721 AAGTTATTTTATATATAATAATATATAATAATAATAATAATAATAATAATAATAATAATA 780	
DB		
DB	35103 AAGTTATTTTATATATAATAATATATAATAATAATAATAATAATAATAATAATAATAATA 35162	
QY	781 TGTGTGTGTATGCGT 840	
DB		
DB	35163 TGT 35222	
QY	841 AGCCATTTCTAGAGCTTGTATGGTTATCGAGGTCTGACTAGGCGATGATTTTCCAGGAGCA 900	
DB		
DB	35223 AGCCATTTCTAGAGCTTGTATGGTTATCGAGGTCTGACTAGGCGATGATTTTCCAGGAGCA 35282	
QY	901 AGATTGGCATATCATTTGTAACTAAAGAGCTGACATTTGACCCAGACATATTTGTACTCTTT 960	
DB		

Db	35283	AGATTGGCATATCATTTGTAACTTAAAAAGCTGACATTGACCGCAGACATATTGTACTCTTT	35342
Qy	961	CTAAAAATAATAATAATGCTTAAACAGAAAGAGAACCGTTCGTTTGGCAATCTACAG	1020
Db	35343	CTAAAAATAATAATAATGCTTAAACAGAAAGAGAGAACCGTTCGTTTGGCAATCTACAG	35402
Qy	1021	CTAGTTAGAGACTTTGAGGAAGAAATTCACACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAAGC	1080
Db	35403	CTAGTTAGAGACTTTGAGGAAGAAATTCACACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAAGC	35462
Qy	1081	AAGAAGTTGAAGTTGCTTACAGCCAGAGGACATAAAGTATCATGTCTCCTTTAACTAGCATATA	1140
Db	35463	AAGAAGTTGAAGTTGCTTACAGCCAGAGGACATAAAGTATCATGTCTCCTTTAACTAGCATATA	35522
Qy	1141	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAAATCAGCCAACT	1200
Db	35523	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAAATCAGCCAACT	35582
Qy	1201	AAGTTGTCCTTTTCTCGTTTCGTTTCCACCATGGAAACATTTTGTATTAGTTAATCTCTTC	1260
Db	35583	AAGTTGTCCTTTTCTCGTTTCGTTTCCACCATGGAAACATTTTGTATTAGTTAATCTCTTC	35642
Qy	1261	TATCTTGAATCTT	1273
Db	35643	TATCTTGAATCTT	35655

RESULT 6

RESOLU 6
ABN95627

ID ABN95627 standard; DNA: 38059 BP.

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72065894

AC ABN95627;

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DT 13-AUG-2002 (first entry)

XX

DE Gene #2125 used to diagnose liver cancer.

XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.

XX

OS Homo sapiens.

XX

PN WO200229103-A2.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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PD 11-APR-2002.

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PF 02-OCT-2001; 2001WO-US030589.

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PR 02-OCT-2000; 2000US-0237054P.
yy

XX
PA (GENE-) GENE LOGIC INCPA (GENE-) GENE LOGIC INC.
XX

XX
PT Horne D. Alvarez C. Perez-D

PI ROHNE D, ALVARES C, PERES-DA-SILVA S, VOCKLEY JG, XX

DR WPI: 2002-426119/45.

XX
XX
07/07/2007 13:54

PT Diagnosing and detecting the progression of liver ca

PT diagnosis or detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.

XX

PS Claim 1; SEQ ID NO 2125; 298pp; English.

XX

CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver

CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC <http://wipo.int/pub/published/pct/sequences>

SQ Sequence 38059 BP; 12326 A; 7337 C; 7441 G; 10895 T; 0 U; 0 Other;
Query Match 100.0%; Score 1273; DB 6; Length 38059;
Best Local Similarity 100.0%; Pred. No. 1.6e-278;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35283 AGATTGGCATATCATTTGTAACATAAAAAAGCTGACATTGACCCAGACATATTTGTAATCTTTT 35342
Qy 961 CTAAAAATATATATATATGCTTAACAGAAAGAGAGACCGTTGCTTTGCAATCTACAG 1020
Db 35343 CTAAAAATATATATATATGCTTAACAGAAAGAGAGACCGTTGCTTTGCAATCTACAG 35402
Qy 1021 CTAGTAGAGACTTTGAGGAGAAATCAACAGTGTGCTTTTCCAGCAGTGTTCAGAGCCCAAGC 1080
Db 35403 CTAGTAGAGACTTTGAGGAGAAATCAACAGTGTGCTTTTCCAGCAGTGTTCAGAGCCCAAGC 35462
Qy 1081 AAGAAGTTGAAGTTGCTTAGACAGAGGACATATGCTCTCTTTTAACTAGCATTA 1140
Db 35463 AAGAAGTTGAAGTTGCTTAGACAGAGGACATATGCTCTCTTTTAACTAGCATTA 35522
Qy 1141 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGCGATTAAGTCATTTCCCAATCAGCCAACT 1200
Db 35523 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGCGATTAAGTCATTTCCCAATCAGCCAACT 35582
Qy 1201 AAGTTCTCTCTTTCTCTGTTTCCCATGGAACATTTTGATTATATAGTTAACTCTTC 1260
Db 35583 AAGTTCTCTCTTTCTCTGTTTCCCATGGAACATTTTGATTATATAGTTAACTCTTC 35642
Qy 1261 TATCTTGAATCTT 1273
Db 35643 TATCTTGAATCTT 35655

RESULT 7
ADD71098
ID ADD71098 standard; DNA; 38059 BP.
XX
AC ADD71098;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human coagulation factor IX gene SEQ ID NO:102.
XX
KW liver cancer; chronic hepatitis; cirrhosis; liver disease; hepatotropic;
KW cytostatic; gene therapy; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003061564-A2.
XX
PD 31-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-US040718.
XX
PR 21-DEC-2001; 2001US-0341815P.
PR 31-DEC-2001; 2001US-0343185P.
XX
XX (GENE-) GENE LOGIC INC.
PA (LGBI-) LG BIOMEDICAL INST.
XX
XX Koh SS, Liu Q, Chung H, Zeng W, Lee B, Yeramilli S, Song SY;
XX WPI; 2003-663343/62.
XX
XX Diagnosing liver cancer cells, useful for treating liver cancer
PT associated with chronic hepatitis or cirrhosis comprises detecting the
PT level of expression in a tissue sample of one or more genes associated
PT with cancerous liver tissues.
XX
PS Claim 1; SEQ ID NO 102; 176pp; English.
XX
CC The present invention describes a method for diagnosing liver cancer
CC cells comprising detecting the level of expression in a tissue sample of
CC one or more genes given in the specification (see ADD70997 to ADD71105),
CC where differential expression of the genes is indicative of liver cancer.
CC Also described: (1) detecting the progression of liver cancer in a
CC patient; (2) monitoring the treatment of a patient with liver cancer; (3)
CC treating a patient with liver cancer; (4) typing a liver disease in a

CC patient; (5) detecting the presence or progression of liver cancer in a
CC patient with chronic hepatitis or cirrhosis; (6) differentiating liver
CC cancer related to chronic hepatitis from liver cancer related to
CC cirrhosis; (7) screening for an agent capable of modulating the onset or
CC progression of liver cancer; (8) a composition comprising at least two
CC oligonucleotides comprising a sequence that specifically hybridizes to
CC any of the genes; (9) a solid support comprising the at least two
CC oligonucleotides; (10) a computer system comprising a database containing
CC information identifying the level in liver tissue of a set of genes; (11)
CC a method for using the computer system to present information identifying
CC the expression level in tissue or cell of any of the genes; and (12) a
CC therapeutic agent for slowing or halting the progression of liver cancer.
CC The methods are useful for treating liver cancer associated with chronic
CC hepatitis or cirrhosis. The present sequence represents a specifically
CC claimed human gene sequence which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other;
Query Match 100.0%; Score 1273; DB 10; Length 38059;
Best Local Similarity 100.0%; Pred. No. 1.6e-278; Mismatches 0; Gaps 0;
Matches 1273; Conservative 0; Indels 0; Gaps 0;
Qy 1 GGCCTCTCACAACTAATCACCTTTCCCATCTTTTGTAGATTGAATATATATATCTAT 60
Db 34383 GGCCTCTCACAACTAATCACCTTTCCCATCTTTTGTAGATTGAATATATATATCTAT 34442
Qy 61 GATCATTTGCTTTTCTTTTACAGGGGAGAAATTCATATTTTACCTGAGCAATGATTA 120
Db 34443 GATCATTTGCTTTTCTTTTACAGGGGAGAAATTCATATTTTACCTGAGCAATGATTA 34502
Qy 121 GAAATGGAACCACTAGAGGAATAATCTGTGTAGAAATACAGTCATTCTTAAGGGCC 180
Db 34503 GAAATGGAACCACTAGAGGAATAATCTGTGTAGAAATACAGTCATTCTTAAGGGCC 34562
Qy 181 CAGCCCTTGACAAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 240
Db 34563 CAGCCCTTGACAAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 34622
Qy 241 TCACATATGGCAACTAATCACTCACTCAATTTTCCCTCTTACAGAGCATTCATCTCCGAT 300
Db 34623 TCACATATGGCAACTAATCACTCACTCAATTTTCCCTCTTACAGAGCATTCATCTCCGAT 34682
Qy 301 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATAGTTTCTGTATACAGTACAGGATC 360
Db 34683 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATAGTTTCTGTATACAGTACAGGATC 34742
Qy 361 TTTGTTCTACTCTATCACAAGGCCAGTACCACTCATGAAGAAAGAACACAGGAGTAGC 420
Db 34743 TTTGTTCTACTCTATCACAAGGCCAGTACCACTCATGAAGAAAGAACACAGGAGTAGC 34802
Qy 421 TGAGAGGCTAAACATCATCAAAAAACACTACTCTTTTCTCTACCCCTATTCCTCAATCTT 480
Db 34803 TGAGAGGCTAAACATCATCAAAAAACACTACTCTTTTCTCTACCCCTATTCCTCAATCTT 34862
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 540
Db 34863 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 34922
Qy 541 TTTTACCCTTCCATGCTGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTTCTGTA 600
Db 34923 TTTTACCCTTCCATGCTGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTTCTGTA 34982
Qy 601 CACAGTTATACATGCTATCAAAACCCAGACTTGTCTCCATAGTGAGACTTCGTTTTCAG 660
Db 34983 CACAGTTATACATGCTATCAAAACCCAGACTTGTCTCCATAGTGAGACTTCGTTTTCAG 35042
Qy 661 AACATAGGAGTCAAGTAAAGTCCCTGAAAAGTTTGGGGAAAAGTTTCTTTTCAGAGATT 720
Db 35043 AACATAGGAGTCAAGTAAAGTCCCTGAAAAGTTTGGGGAAAAGTTTCTTTTCAGAGATT 35102
Qy 721 AAGTTATTTATATATATATATATATATAAATAATATATAAATAAATAATATATAG 780
Db AAGTTATTTATATATATATATATATATAAATAATATATAAATAAATAATATATAG

The invention relates to nucleic acid sequences which regulate gene expression in an age-related manner and/or in a liver-specific manner. The invention identifies regions of the human factor IX (hFIX) gene, and a region of the human protein C (hPC) gene, which are age-related regulatory sequences. The hFIX age-related regulatory sequences are designated AES' (AAAF54016) and AES' (AAAF54017) and are found in the 5' UTR (at position 2164-2165 of AAAF54018) and 3' UTR (at position 34383-35655 of AAAF54018) respectively. These elements act synergistically to increase hFIX levels over the lifespan of an individual; however, they can independently exert effects on hFIX mRNA in an age-related manner, with AES' acting to stabilise hFIX mRNA, and AES' acting to increase hFIX mRNA levels, over time. AES' also directs liver-specific expression. The hPC gene age-related regulatory sequence is found in the 5' UTR

CC (AAF54081), and contains two PBA-3 (polyoma virus activator 3) elements
CC 5'-GAGGAAA-3' and 5'-CAGGAAG-3'. The age-related regulatory sequences of
CC the invention, along with their homologues, variants and fragments, may
CC be used in the construction of recombinant expression vectors for the
CC expression of a desired sequence in an age-related fashion in a host
CC cell. Preferred target genes for expression in such age-regulatable
CC expression vectors include those encoding proteins involved in blood
CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
CC anti-coagulants protein C and antithrombin III), human alpha-1-
CC antitrypsin, PEA-3 protein and reporter proteins such as luciferase.
CC Preferred promoters for use in such age-regulatable expression vectors
CC include the human factor IX promoter, the T7 promoter, the T3 promoter
CC and the SP6 promoter. The expression vectors of the invention may be used
CC in gene therapy to provide age-related and/or liver-specific expression
CC of target genes. Age-regulatable constructs may be used in the treatment
CC of such age-related conditions such as thrombosis, cardiovascular
CC disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,
CC osteoporosis, osteoarthritis and dementia. Specifically, they may be used
CC to express factor IX antisense mRNA in the treatment of thrombotic
CC conditions associated with the natural age-related rise in factor IX
CC expression. Transgenic cells or animals that contain vectors of the
CC invention are useful as models of these diseases, in screening for
CC potential therapeutic agents and for studying normal processes such as
CC ageing and gene expression. Fragments and homologues of age-related
CC regulatory sequences, are useful as probes to detect, isolate or identify
CC other such sequences in samples. The present sequence represents an AE3'
CC region homologue

XX Sequence 1273 BP; 392 A; 262 C; 218 G; 401 T; 0 U; 0 Other;

Query Match 99.9%; Score 1271.4; DB 4; Length 1273;
Best Local Similarity 99.9%; Pred. No. 1.6e-278;
Matches 1272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCTCTCACTAATCACTTCCCATCTTTTGTAGATTGTAATATATATATCTAT 60
DB 1 GGCCTCTGACTAACTAATCACTTCCCATCTTTTGTAGATTGTAATATATATATCTAT 60
QY 61 GATCATTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA 120
DB 61 GATCATTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA 120
QY 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTCAGTCATTCTTAAGGGCC 180
DB 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTCAGTCATTCTTAAGGGCC 180
QY 181 CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC 240
DB 181 CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC 240
QY 241 TCCACTATGCGCACTAATCACTCAATTTTCCCTCTTAGCAGCATTCCTCCGAT 300
DB 241 TCCACTATGCGCACTAATCACTCAATTTTCCCTCTTAGCAGCATTCCTCCGAT 300
QY 301 CTTCCTTTGCTTCCCAACCAACATCAATGTTTATTAGTCTGTATACAGTACAGGATC 360
DB 301 CTTCCTTTGCTTCCCAACCAACATCAATGTTTATTAGTCTGTATACAGTACAGGATC 360
QY 361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420
DB 361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420
QY 421 TGAGAGGCTAAACTCATCAAAAACACTACTCTTTTCTTACCCCTATTCTCAATCTT 480
DB 421 TGAGAGGCTAAACTCATCAAAAACACTACTCTTTTCTTACCCCTATTCTCAATCTT 480
QY 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTTCTTCTTCTTCTTCTTCTTCTCC 540
DB 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTTCTTCTTCTTCTTCTTCTTCTCC 540
QY 541 TTTTACCCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCTTCTGTTATATCTCTGTA 600
DB 541 TTTTACCCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCTTCTGTTATATCTCTGTA 600

QY 601 CACAGTTATACATGCTCTATCAAAACCCAGACTTGCTTCCATAGTGAGACTTCTCTTTCAG 660
DB 601 CACAGTTATACATGCTCTATCAAAACCCAGACTTGCTTCCATAGTGAGACTTCTCTTTCAG 660
QY 661 AACATAGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
DB 661 AACATAGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
QY 721 AAGTTATTTTATATATATAATATATATAATAATAATAATAATAATAATAATAATAATA 780
DB 721 AAGTTATTTTATATATAATATATATAATAATAATAATAATAATAATAATAATAATAATA 780
QY 781 TGTGTGCTGTATGCTGT 840
DB 781 TGTGTGCTGTATGCTGT 840
QY 841 AGCCATTCTAAGAGCTTCTGTATGTTTATGAGGTCTGTAGGTCATGTTTTCAGGAAGCA 900
DB 841 AGCCATTCTAAGAGCTTCTGTATGTTTATGAGGTCTGTAGGTCATGTTTTCAGGAAGCA 900
QY 901 AGATTGGCATATCATTTGTAACATAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960
DB 901 AGATTGGCATATCATTTGTAACATAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960
QY 961 CTAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1020
DB 961 CTAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1020
QY 1021 CTAGTAGAGACTTTTTCAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCAAGC 1080
DB 1021 CTAGTAGAGACTTTTTCAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCAAGC 1080
QY 1081 AAGAAGTTGAAGTTCCCTTAGACAGGACATTAAGTATCATGCTCTCTTTTAACTAGCATA 1140
DB 1081 AAGAAGTTGAAGTTCCCTTAGACAGGACATTAAGTATCATGCTCTCTCTTTTAACTAGCATA 1140
QY 1141 CCCCAGCTGGAGAGGGTGCAGCAGGCTCAAGGCAATGTCATTCCAATCAGGCAACT 1200
DB 1141 CCCCAGCTGGAGAGGGTGCAGCAGGCTCAAGGCAATGTCATTCCAATCAGGCAACT 1200
QY 1201 AAGTTGTCTTTCTTCTGTTTCTGTTTCCCATGGAACATTTTGTATAGTTAATCCTTC 1260
DB 1201 AAGTTGTCTTTCTTCTGTTTCTGTTTCCCATGGAACATTTTGTATAGTTAATCCTTC 1260
QY 1261 TATCTTGAATCTT 1273
DB 1261 TATCTTGAATCTT 1273

RESULT 11

AAF54075

ID AAF54075 standard; DNA; 1273 BP.

XX

AC AAF54075;

XX

DT 30-MAR-2001 (first entry)

XX

DE hFIX gene AE3' age-related regulatory region homologue, SEQ ID NO:78.

XX

KW Age-related gene regulation; gene expression; human factor IX; hFIX;

KW AE3'; 3' UTR; 3' untranslated region; AE3'' element;

KW age-regulatable expression construct; antisense therapy; gene therapy;

KW thrombosis; cardiovascular disease; diabetes; Alzheimer's disease;

KW Parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia; ds.

XX

OS Homo sapiens.

OS Synthetic.

XX

FN WO200075279-A2.

PD

XX 14-DEC-2000.

XX

PF 06-JUN-2000; 2000WO-US015728.
 PR 09-JUN-1999; 99US-00328925.
 XX (UNMI) UNIV MICHIGAN.
 XX Kurachi K, Kurachi S;
 PI WPI; 2001-061708/07.
 XX
 PT New regulatory elements that control age-related gene expression, useful
 PT in gene therapy and for reducing Factor IX expression.
 XX
 XX Disclosure; Fig 3B; 225pp; English.
 CC The invention relates to nucleic acid sequences which regulate gene
 CC expression in an age-related manner and/or in a liver-specific manner.
 CC The invention identifies regions of the human factor IX (hFIX) gene, and
 CC a region of the human protein C (hPC) gene, which are age-related
 CC regulatory sequences. The hFIX age-related regulatory sequences are
 CC designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'
 CC UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34383-
 CC 35655 of AAF54018) respectively. These elements act synergistically to
 CC increase hFIX levels over the lifespan of an individual; however, they
 CC can independently exert effects on hFIX mRNA in an age-related manner,
 CC with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX
 CC mRNA levels, over time. AE5' also directs liver-specific expression. The
 CC hPC gene age-related regulatory sequence is found in the 5' UTR
 CC (AAF54081), and contains two PEA-3 (polyoma virus activator 3) elements
 CC 5'-GAGGAAA-3' and 5'-CAGGAG-3'. The age-related regulatory sequences of
 CC the invention, along with their homologues, variants and fragments, may
 CC be used in the construction of recombinant expression vectors for the
 CC expression of a desired sequence in an age-related fashion in a host
 CC cell. Preferred target genes for expression in such age-regulatable
 CC expression vectors include those encoding proteins involved in blood
 CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
 CC anti-coagulants protein C and antithrombin III), human alpha-1-
 CC antitrypsin, PEA-3 protein and reporter proteins such as luciferase.
 CC Preferred promoters for use in such age-regulatable expression vectors
 CC include the human factor IX promoter, the T7 promoter, the T3 promoter
 CC and the SP6 promoter. The expression vectors of the invention may be used
 CC in gene therapy to provide age- related and/or liver-specific expression
 CC of target genes. Age-regulatable constructs may be used in the treatment
 CC of such age-related conditions such as thrombosis, cardiovascular
 CC disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,
 CC osteoporosis, osteoarthritis and dementia. Specifically, they may be used
 CC to express factor IX antisense mRNA in the treatment of thrombotic
 CC conditions associated with the natural age-related rise in factor IX
 CC expression. Transgenic cells or animals that contain vectors of the
 CC invention are useful as models of these diseases, in screening for
 CC potential therapeutic agents and for studying normal processes such as
 CC ageing and gene expression. Fragments and homologues of age-related
 CC regulatory sequences, are useful as probes to detect, isolate or identify
 CC other such sequences in samples. The present sequence represents an AE3'
 CC region homologue
 XX
 SQ Sequence 1273 BP; 392 A; 263 C; 217 G; 401 T; 0 U; 0 Other;
 Query Match 99.7%; Score 1269.8; DB 4; Length 1273;
 Best Local Similarity 99.8%; Pred. No. 3.6e-278;
 Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GGCTCTCACTAACTACATTTCCCATCTTTGTTAGATTGGAATATATACATTTCTAT 60
 DB 1 GGCTCTCACTAACTAACTTTCCCATCTTTGTTAGATTGGAATATATACATTTCTAT 60
 QY 61 GATCATTTGTTTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTCATTA 120
 DB 61 GATCATTTGTTTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTCATTA 120
 QY 121 GAAATGGAAACCACTAGAGGAATATAATGTTGTAGGAATATACAGTCATTTCTAAGGGCC 180
 DB 121 GAAATGGAAACCACTAGAGGAATATAATGTTGTAGGAATATACAGTCATTTCTAAGGGCC 180

QY 181 CAGCCCTTGACAAAATTGTGAAGTTAAATTTCTCCACTCTCTCCATCAGATACTATGTTTC 240
 DB 181 CAGCCCTTGACAAAATTGTGAAGTTAAATTTCTCCACTCTCTCCATCAGATACTATGTTTC 240
 QY 241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTCTTAGCAGCATTTCCATCTTCCCGAT 300
 DB 241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTCTTAGCAGCATTTCCATCTTCCCGAT 300
 QY 301 CTTCCTTTGCTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGATC 360
 DB 301 CTTCCTTTGCTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGATC 360
 QY 361 TTTGGTCTACTCTATCAAGGCCAGTACACACTCATGAAGAAAGAACACAGAGTAGC 420
 DB 361 TTTGGTCTACTCTATCAAGGCCAGTACACACTCATGAAGAAAGAACACAGAGTAGC 420
 QY 421 TGAGAGGCTTAAACTCATCAAAAACACTACTCTTTTCTCTTACCTTATTCCTCAATCTT 480
 DB 421 TGAGAGGCTTAAACTCATCAAAAACACTACTCTTTTCTCTTACCTTATTCCTCAATCTT 480
 QY 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 540
 DB 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 540
 QY 541 TTTTACCTCCCATGGTCTGTTAAAGAGAGATGGGAGAGCATCTTCTGTATATCTTCTGTA 600
 DB 541 TTTTACCTCCCATGGTCTGTTAAAGAGAGATGGGAGAGCATCTTCTGTATATCTTCTGTA 600
 QY 601 CACAGTTATACATGCTCTATCAAAACCAGACTTGTCTTCCATAGTGGAGAGCTTGTCTTTCAG 660
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 DB 721 AAGTTATTTTATATATATATATATATAATAATAATAATAATAATAATAATAATAATA 780
 QY 781 TGTGTGTGTATGCTGT 840
 DB 781 TGTGTGTGTATGCTGT 840
 QY 841 AGCCATTCTAAGAGCTTGTATGTTTATGAGGCTGTGCTAGGATCATTTTCACGAGGCA 900
 DB 841 AGCCATTCTAAGAGCTTGTATGTTTATGAGGCTGTGCTAGGATCATTTTCACGAGGCA 900
 QY 901 AGATTGGCATATCATTTGTAATAAAAGCTGACATTTGACCCAGACATATTTGACTCTTT 960
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 QY 961 CTAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1020
 DB 961 CTAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1020
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 DB 1021 CTAGTAGAGACTTTGAGGAGAAATTCACAGTGTGTCTTTTCAGCAGTGTTCAGAGCCNAGC 1080
 QY 1081 AAGAGTTTCAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTTAACTAGCATA 1140
 DB 1081 AAGAGTTTCAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTTAACTAGCATA 1140
 QY 1141 CCCCAGAGTGGAGAGAGGGTGCAGCAGGCTCAAAGGCAATAGTCATTTCCAATCAGCAACT 1200
 DB 1141 CCCCAGAGTGGAGAGAGGGTGCAGCAGGCTCAAAGGCAATAGTCATTTCCAATCAGCAACT 1200
 QY 1201 AAGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGAATATATAGTTAATCTTTC 1260
 DB 1201 AAGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGAATATATAGTTAATCTTTC 1260

Qy	1261	TATCTTGAATCTT	1273	
Db	1261	TATCTTGAATCTT	1273	
RESULT 12				
AA	28626			
ID	AA28626 standard; DNA; 2792 BP.			
XX				
AC	AA28626;			
XX				
DT	07-JUN-1999 (first entry)			
XX				
DE	Nucleotide sequence of human factor IX-R338A.			
XX				
KW	Human; Factor IX-R338A; substitution; Factor X; Factor Xa;			
KW	mammalian blood coagulation cascade; phospholipid surface; calcium ion;			
KW	Factor VIIa; blood clotting; haemophilia B; ss.			
XX				
OS	Homo sapiens.			
OS	Synthetic.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	156..1423		
FT		/*tag= a		
FT		/product= "Factor IX-R338A"		
XX				
PN	WO9903496-A1.			
XX				
PD	28-JAN-1999.			
XX				
PF	17-JUL-1998; 98WO-US014750.			
XX				
PR	21-JUL-1997; 97US-0053571P.			
XX				
PA	(UYN-) UNIV NORTH CAROLINA.			
PA	(STAF/) STAFFORD D W.			
PA	(CHAN/) CHANG J L.			
XX				
PI	Stafford DW, Chang JL;			
XX				
DR	WPI; 1999-131867/11.			
DR	P-PSDB; AAY03203.			
XX				
PT	Factor IX antihemophilic factor with increased clotting activity - due to			
PT	an amino acid substitution (of arginine) at position 338.			
XX				
PS	Disclosure; Page 26-32; 38pp; English.			
XX				
CC	This is the nucleotide sequence encoding a non-naturally occurring human			
CC	Factor IX-R338A protein having an amino acid substitution at amino acid			
CC	position 338 of arginine to alanine. Factor IX converts Factor X to			
CC	Factor Xa in the mammalian blood coagulation cascade, in a process that			
CC	requires a phospholipid surface, calcium ions and Factor VIIa. Nucleic			
CC	acids encoding Factor IX can be used to facilitate blood clotting, e.g.			
CC	in patients afflicted with haemophilia B			
XX				
SQ	Sequence 2792 BP; 858 A; 541 C; 569 G; 824 T; 0 U; 0 Other;			
Query Match				
Best Local Similarity 99.7%; Score 1269.8; DB 2; Length 2792;				
Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	1	GGCTCTCACTAACTAATCACCTTCCCATCTTTGTAGATTGAATATATATATCTAT	60	
Db	1452	GGCTCTCACTAACTAATCACCTTCCCATCTTTGTAGATTGAATATATATATCTAT	1511	
Qy	61	GATCATTGCTTTTCTCTTTACAGGGGAGAATTTTCATATTTTACCTGACCAATTTGATTA	120	
Db	1512	GATCATTGCTTTTCTCTTTACAGGGGAGAATTTTCATATTTTACCTGACCAATTTGATTA	1571	
Qy	121	GAATAATGGAACCACTAGAGGAATATAATGTGTAGGAATTTACAGTCATTTCTAAGGGCC	180	

Db	1572	GAATAATGGAACCACTAGAGGAATATAATGTGTAGGAATTTACAGTCATTTCTAAGGGCC	1631	
QY	181	CAGCCCTTGACAAAAATGTGAAGTTAAATCTCCACTCTGTCCATCAGATATATGGTTTC	240	
Db	1632	CAGCCCTTGACAAAAATGTGAAGTTAAATCTCCACTCTGTCCATCAGATATATGGTTTC	1691	
QY	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCAATCCATCTTCCGAT	300	
Db	1692	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCAATCCATCTTCCGAT	1751	
QY	301	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	360	
Db	1752	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	1811	
QY	361	TTTGGTCTACTCTATCAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC	420	
Db	1812	TTTGGTCTACTCTATCAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC	1871	
QY	421	TGAGAGGCTAAACCTCATCAAAACACACTCTCTTTCTCTACCTATTCTCAATCTT	480	
Db	1872	TGAGAGGCTAAACCTCATCAAAACACACTCTCTTTCTCTACCTATTCTCAATCTT	1931	
QY	481	TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTCTTACTCCCTCTCTCC	540	
Db	1932	TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTCTTACTCCCTCTCTCC	1991	
QY	541	TTTTACCTTCCATGGTCTGTTAAAGGAGAGATGGGGAGCATCATCTGTATATATCTCTGA	600	
Db	1992	TTTTACCTTCCATGGTCTGTTAAAGGAGAGATGGGGAGCATCATCTGTATATATCTCTGA	2051	
QY	601	CACAGTTATACATGCTATCAAAACCCAGACTGCTTCCATAGTGAGACTTCTTTTTCAG	660	
Db	2052	CACAGTTATACATGCTATCAAAACCCAGACTGCTTCCATAGTGAGACTTCTTTTTCAG	2111	
QY	661	AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGAAAAGTTTCTTTTCAGAGATT	720	
Db	2112	AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGAAAAGTTTCTTTTCAGAGATT	2171	
QY	721	AAGTTATTTTATATATATATATATATAATAATAATAATAATAATAATAATAATAATA	780	
Db	2172	AAGTTATTTTATATATATATATATATAATAATAATAATAATAATAATAATAATAATA	2231	
QY	781	TGTGTGTGTGTATGCTGTGTGTAGACACACACGATACACACATATATATGAAGCAATA	840	
Db	2232	TGTGTGTGTGTATGCTGTGTGTAGACACACACGATACACACATATATATGAAGCAATA	2291	
QY	841	AGCCATTCTAAGAGCTTGTATGGAGTCTGACTAGGCATGATTTACAGAGGCA	900	
Db	2292	AGCCATTCTAAGAGCTTGTATGGAGTCTGACTAGGCATGATTTACAGAGGCA	2351	
QY	901	AGATTGGCATATCATTTGTAACATAAAAAAGCTGACATTGACCCAGACATATTTGACTCTTT	960	
Db	2352	AGATTGGCATATCATTTGTAACATAAAAAAGCTGACATTGACCCAGACATATTTGACTCTTT	2411	
QY	961	CTAAAAATAATAATAATAATGCTAACAGAAAGAGAACCGTTCGTTTGCATCTACAG	1020	
Db	2412	CTAAAAATAATAATAATAATGCTAACAGAAAGAGAACCGTTCGTTTGCATCTACAG	2471	
QY	1021	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTCTCTTACAGCAGTGTTCAGAGCCAAGC	1080	
Db	2472	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTCTCTTACAGCAGTGTTCAGAGCCAAGC	2531	
QY	1081	AAGAAAGTTGAAGTTGCCCTAGACCAGGACATAGATATCATGTCTCTTTTAACTAGCATA	1140	
Db	2532	AAGAAAGTTGAAGTTGCCCTAGACCAGGACATAGATATCATGTCTCTTTTAACTAGCATA	2591	
QY	1141	CCCCCAAGTGGAGAGGGTGCAGAGGCTCAAGGCATAAGTCATTCCAAATCAGCAACT	1200	
Db	2592	CCCCCAAGTGGAGAGGGTGCAGAGGCTCAAGGCATAAGTCATTCCAAATCAGCAACT	2651	
QY	1201	AAGTTGTCTCTTTTCTGGTTTCTGTTCACCATGGAACATTTTGAATTATAGTTTAACTCTTC	1260	
Db	2652	AAGTTGTCTCTTTTCTGGTTTCTGTTCACCATGGAACATTTTGAATTATAGTTTAACTCTTC	2711	

Db 2544 AAGAAGUUAAGUCCUAGACAGGAGCAUAAGUAUCAUGUCCUUAUACUAGCAUA 2603

Qy 1141 CCCGAAGTGGAGAGGGTGCAGCAGGCTCAAAAGGCATAGTCAATCCATCAGCAACT 1200

Db 2604 CCCGAAGUGAGAGGGUGCAGCAGGCUCAAGGCAUAGUUAUCCAUAGCCACU 2663

Qy 1201 AAGTTGCTCTTCTGTTGTTGTTGCACATCGAATTTGATATATAGTTAATCCTTC 1260

Db 2664 AAGUUGUCCUUAUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGU 2723

Qy 1261 TATCTTGAATCTT 1273

Db 2724 UAUUGUUAUUCU 2736

RESULT 15

AAF54076

ID AAF54076 standard; DNA; 1273 BP.

XX AAF54076;

XX

30-MAR-2001 (first entry)

XX

DE hFIX gene AE3' age-related regulatory region homologue, SEQ ID NO:79.

XX

KW Age-related gene regulation; gene expression; human factor IX; hFIX;

KW AE3'; 3' UTR; 3' untranslated region; AE3'; element;

KW age-regulatable expression construct; antisense therapy; gene therapy;

KW thrombosis; cardiovascular disease; diabetes; Alzheimer's disease;

KW Parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia; ds.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200075279-A2.

XX

PD 14-DEC-2000.

XX

PF 06-JUN-2000; 2000WO-US015728.

XX

PR 09-JUN-1999; 99US-00328925.

XX

PA (UNMI) UNIV MITCHIGAN.

XX

PI Kurachi K, Kurachi S;

XX

DR WPI; 2001-061708/07.

XX

PT New regulatory elements that control age-related gene expression, useful

PT in gene therapy and for reducing Factor IX expression.

XX

PS Disclosure; Fig 3C; 225pp; English.

XX

CC The invention relates to nucleic acid sequences which regulate gene

CC expression in an age-related manner and/or in a liver-specific manner.

CC The invention identifies regions of the human factor IX (hFIX) gene, and

CC a region of the human protein C (hPC) gene, which are age-related

CC regulatory sequences. The hFIX age-related regulatory sequences are

CC designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'

CC UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34383-

CC 35655 of AAF54018) respectively. These elements act synergistically to

CC increase hFIX levels over the lifespan of an individual; however, they

CC can independently exert effects on hFIX mRNA in an age-related manner.

CC with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX

CC mRNA levels, over time. AE5' also directs liver-specific expression. The

CC hPC gene age-related regulatory sequence is found in the 5' UTR

CC (AAF54081), and contains two PEA-3 (polyoma virus activator 3) elements

CC 5'-GAGGAAA-3' and 5'-CAGGAAG-3'. The age-related regulatory sequences of

CC the invention, along with their homologues, variants and fragments, may

CC be used in the construction of recombinant expression vectors for the

CC expression of a desired sequence in an age-related fashion in a host

CC cell. Preferred target genes for expression in such age-regulatable

CC expression vectors include those encoding proteins involved in blood

CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the

CC anti-coagulants protein C and antithrombin III), human alpha-1-

CC antitrypsin, PEA-3 protein and reporter proteins such as luciferase.

CC Preferred promoters for use in such age-regulatable expression vectors

CC include the human factor IX promoter, the T7 promoter, the T3 promoter

CC and the SP6 promoter. The expression vectors of the invention may be used

CC in gene therapy to provide age-related and/or liver-specific expression

CC of target genes. Age-regulatable constructs may be used in the treatment

CC of age-related conditions such as thrombosis, cardiovascular

CC disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,

CC osteoporosis, osteoarthritis and dementia. Specifically, they may be used

CC to express factor IX antisense mRNA in the treatment of thrombotic

CC conditions associated with the natural age-related rise in factor IX

CC expression. Transgenic cells or animals that contain vectors of the

CC invention are useful as models of these diseases, in screening for

CC potential therapeutic agents and for studying normal processes such as

CC ageing and gene expression. Fragments and homologues of age-related

CC regulatory sequences, are useful as probes to detect, isolate or identify

CC other such sequences in samples. The present sequence represents an AE3',

CC region homologue

XX

SQ Sequence 1273 BP; 392 A; 263 C; 217 G; 401 T; 0 U; 0 Other;

Query Match 99.5%; Score 1266; DB 4; Length 1273;

Best Local Similarity 99.7%; Pred. No. 1.9e-277;

Matches 1269; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGCCTCTCACTAACTAACTCACTTCCCATCTTTGTTAGATTTGAATATATACATCTAT 60

Db 1 GGCCTCTCACTAACTAACTCACTTCCCATCTTTGTTAGATTTGAATATATACATCTAT 60

Qy 61 GATCATTGCTTTTCTCTTTTACAGGGGAGAAATTTCAATATTTTACCTGAGCAAAATGATTA 120

Db 61 GATCATTGCTTTTCTCTTTTACAGGGGAGAAATTTCAATATTTTACCTGAGCAAAATGATTA 120

Qy 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTCTTAAGGGCC 180

Db 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTCTTAAGGGCC 180

Qy 181 CAGCCCTTCACAAAATTTGAAAGTTAAATTTGCTCCACTCTGCCATCAGATCTATGGTTC 240

Db 181 CAGCCCTTCACAAAATTTGAAAGTTAAATTTGCTCCACTCTGCCATCAGATCTATGGTTC 240

Qy 241 TCACATATGGCAACTAACTCACTCAATTTTCCCTCTTAGCAGCATTTCATCTCCCGAT 300

Db 241 TCACATATGGCAACTAACTCACTCAATTTTCCCTCTTAGCAGCATTTCATCTCCCGAT 300

Qy 301 CTTCTTTGCTTCTCCAAACCAAAACATCAATGTGTTATTAGTTCTGTATACAGTACAGGATC 360

Db 301 CTTCTTTGCTTCTCCAAACCAAAACATCAATGTGTTATTAGTTCTGTATACAGTACAGGATC 360

Qy 361 TTTGGTCTACTCTATCACAAGGCCAGTACACACTCATGAAAGAAACACAGAGGATGAGC 420

Db 361 TTTGGTCTACTCTATCACAAGGCCAGTACACACTCATGAAAGAAACACAGAGGATGAGC 420

Qy 421 TCAGAGGCTTAAACACTCATCAAAAACACTACTCTTTTCCCTCTTACCCCTCTCTCCC 480

Db 421 TCAGAGGCTTAAACACTCATCAAAAACACTACTCTTTTCCCTCTTACCCCTCTCTCCC 480

Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCTT 540

Db 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCTT 540

Qy 541 TTTTACCTTCCATGGTCTGTTAAAGGAGAGATGGGAGCATCATCTGTTATATCTTCTGTA 600

Db 541 TTTTACCTTCCATGGTCTGTTAAAGGAGAGATGGGAGCATCATCTGTTATATCTTCTGTA 600

Qy 601 CACAGTTATACATGCTATCAAAACCAGACTTGTCTCCATAGTGGAGACTGCTTTTCAG 660

Db 601 CACAGTTATACATGCTATCAAAACCAGACTTGTCTCCATAGTGGAGACTGCTTTTCAG 660

Qy 661 AACATAGGATGAAGTAAAGGTCCTGAAAGTTTGGGGGAAAGTTTCTTTTTCAGAGATT 720

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OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 13:51:23 ; Search time 5457 Seconds
(without alignments)
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- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1273	100.0	1273	6	AR390766
2	1273	100.0	1707	6	AX379348 Sequence
3	1273	100.0	2775	6	AR178034 Sequence
4	1273	100.0	2775	9	HUMCIX
5	1273	100.0	2775	11	G28615
6	1273	100.0	2804	6	CQ882048
7	1273	100.0	2804	6	AR452580
8	1273	100.0	38059	6	AR390767
9	1273	100.0	38059	6	AX409478
10	1273	100.0	38059	9	HUMFIXG
11	1272	99.9	1272	6	AR390828
12	1271.4	99.9	1273	6	AR390821
13	1271.4	99.9	1273	6	AR390822
14	1271.4	99.9	35458	9	AF536327
15	1269.8	99.7	1273	6	AR390823
16	1269.8	99.7	2802	6	A47227
17	1269.8	99.7	3121	9	HUMFIXG6
18	1268.2	99.6	2781	6	HSFACIXM
19	1266.6	99.5	1273	6	AR390824

20	1261	99.1	1272	6	AR390827
21	1261	99.1	1275	6	AR390825
22	1260	99.0	1276	6	AR390826
23	1257.4	98.8	158557	9	HS88D7
24	1230.6	96.7	2775	6	CQ714145
25	1186.4	93.2	2340	6	A47229
26	1151.6	90.5	1361	6	I01257
27	1023	80.4	1023	11	G10618
28	921.4	72.4	3130	9	S66752
29	883.4	69.4	1971	6	CQ216726
30	883.4	69.4	1971	6	CQ255295
31	272.6	21.4	2869	4	DOGFIX
32	261	20.5	3080	4	DOGFIXA
33	186	14.6	1438	6	AX662323
34	186	14.6	1639	6	A01819
35	186	14.6	1639	6	A13997
36	186	14.6	1639	6	A14017
37	186	14.6	1639	9	HUMFIXA
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39	175.8	13.8	2705	4	AY461381S6
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43	110	8.6	1610	6	AR202300
44	109	8.6	1548	6	AR008972
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ALIGNMENTS

RESULT 1
AR390766
LOCUS AR390766 1273 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6610906.
ACCESSION AR390766
VERSION AR390766.1 GI:40113107
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1273)
AUTHORS Kurachi, K. and Kurachi, S.
TITLE Nucleotide sequences for gene regulation and methods of use thereof
JOURNAL Patent: US 6610906-A 3 26-AUG-2003;
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ORIGIN

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Db	1	GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTAGATTTGAATATATACATCTAT	60	
QY	61	GATCATTTGCTTTTCTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATTCATTA	120	
Db	61	GATCATTTGCTTTTCTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATTCATTA	120	
QY	121	GAATAATGGAACCACTAGAGGAATATATGTTTAGAAATTTACAGTCATTTCTTAAGGGCC	180	
Db	121	GAATAATGGAACCACTAGAGGAATATATGTTTAGAAATTTACAGTCATTTCTTAAGGGCC	180	
QY	181	CAGCCCTTGACAAAATTTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC	240	
Db	181	CAGCCCTTGACAAAATTTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC	240	
QY	241	TCACATATGGCAACTAACTCACTCAATTTTCCCTCTCTAGCAGCATTTCATCTCCGAT	300	
Db	241	TCACATATGGCAACTAACTCACTCAATTTTCCCTCTCTAGCAGCATTTCATCTCCGAT	300	

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Qy 301 CTTCTTTGCTTCCCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
Db 301 CTTCTTTGCTTCCCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
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Db 781 TGTGTGTGTATGCGTGTGTGTAGACACACAGCATACACATATAATATGAAGCAATA 840
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Qy 1261 TATCTTGAATCTT 1273
Db 1261 TATCTTGAATCTT 1273

LOCUS AX379348 1707 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 7 from Patent WO0198482.
ACCESSION AX379348
VERSION AX379348.1 GI:19575188
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Miao,C.H. and Kay,M.A.
TITLE Liver-specific gene expression cassettes, and methods of use
JOURNAL Patent: WO 0198482-A 7 27-DEC-2001;
The Board of Trustees of The Leland Stanford Junior University (US)
; The University of Washington (US)
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 1273; DB 6; Length 1707;
Best Local Similarity 100.0%; Pred. No. 2.4e-261;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTGTAGATTGGAATATATACATCTAT 60
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Qy 61 GATCAATTCGTTTCTCTTTACAGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA 120
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Db 171 GAAATGGAACCACTAGAGGAATAATGTTGTAGGAAATTACAGTCAATTTCTAAGGGCC 230
Qy 181 GAGCCCTTGACAAAATTGTGAAGTTAAATTCCTCACTCTGTCCTCAGTACTATGTTTC 240
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Qy 241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCTCCGAT 300
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Qy 301 CTTCTTTGCTTCTCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
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Qy 361 TTTGCTCTACTCTATCACAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420
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Db 471 TGAGAGGCTTAAACTCATCAAAACACACTCTCTTTTCTCTTACTCTCTCTCTCCC 530
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Db 531 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTTCTTCTTACTCCCTCTCTCCC 590
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Qy 661 AACATAGGATGAAGTAAAGTGGCTGCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGATT 720
Db 711 AACATAGGATGAAGTAAAGTGGCTGCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGATT 770

[illegible]

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA

Tel: 4157259687
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Email: myers@shqc.stanford.edu

Primer A: GTAAGTGCTGAAAGTTGG
Primer B: GTGAAATCATGCCTAGTCAGACC

STS size: 219
PCR profile:

Initial incubation:	94 degrees C for 90 seconds
Denaturation:	94 degrees C for 15 seconds
Annealing:	62 degrees C for 23 seconds
Polymerization:	72 degrees C for 30 seconds
PCR Cycles:	30
Thermal Cycler:	Perkin Elmer 9500

Protocol:									
Template:	25 ng								
Primer:	each 1 uM								
dNTPs:	each 200 uM								
Taq Polymerase:	0.05 units/ul								
Total Vol:	10 ul								
Buffer:									
MgCl2:	2.5 mM								
KCl:	50 mM								
Tris-HCl:	20 mM								
pH:	8.3								
Prepared with primer pairs provided by Sandoz, derived from M11309									
-- Washington University/Merck EST sequence.									
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Best Local Similarity	100.0%;	Pred. No. 2.3e-261;							
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Db	1615	CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC	1679						
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Qy	361	TTTGGTCTACTCTATCACAAGGGCCAGTACCACACTCATGAAGAAGAAACACAGGAGTAGC	420						
Db	1795	TTTGGTCTACTCTATCACAAGGGCCAGTACCACACTCATGAAGAAGAAACACAGGAGTAGC	1859						
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Qy	541	TTTTACCTCCATGGTCGTTTAAAGGAGAGATGGGGAGCATCATTTCTGTATACTTCTGTGA	600						
Db	1975	TTTTACCTCCATGGTCGTTTAAAGGAGAGATGGGGAGCATCATTTCTGTATACTTCTGTGA	2034						
Qy	601	CACAGTTATACATGTCTATCAAAACCCAGACTTGTCTCCATAGTGGAGACTTGTCTTTTCAG	660						
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Qy	61	GATCATTTGCTTTTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTA	120
Db	34443	GATCATTTGCTTTTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTA	34502
Qy	121	GAAATGGAAACCACTAGAGGAATATAATGTGTAGGAATTTACAGTTAACTTCTTAAGGGCC	180
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Qy	421	TGAGAGGCTAAACTCATCAAAAACACTACTCTTTTCTTCTTACCTTATTCCTCAATCTT	480
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Qy	481	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC	540
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Qy	901	AGATTGGCATATCATTTGAACATAAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	960
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Db	35523	CCCCCAAGTGGAGAGGTCGACGAGGCTCAAGGCATTAAGTCATTCATCAGCCAAT	35582
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RESULT 9			
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LOCUS		38059 bp DNA linear PAT 14-JUN-2002	
DEFINITION		Sequence 2125 from Patent WO229103.	
ACCESSION		AX409478	
VERSION		AX409478.1 GI:21442183	
KEYWORDS			
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1	
AUTHORS		Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J. G.	
TITLE		Gene expression profiles in liver cancer	
JOURNAL		Patent: WO 0229103-A 2125 11-APR-2002;	
		GENE LOGIC INC (US)	
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Query Match		100.0%;	Score 1273; DB 6; Length 38059;
Best Local Similarity		100.0%;	Pred. No. 1.9e-261;
Matches 1273;		Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	GGCCTCTCACTAACTACATTTCCCATCTTTTGGTAGAATTTGAATATATACATTTCTAT	60
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Db	34623	TTGGTCTACTCTATCACAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC	34682

QY	301	CTTCTTTGGTCTTCCAAACCAAAACATCAATGTTTATTAGTCTCTGTATACAGTACAGGATC	360
Ds	34683	CTTCTTTGGTCTTCCAAACCAAAACATCAATGTTTATTAGTCTCTGTATACAGTACAGGATC	34742
QY	361	TTTGGTCTACTCTATCAGAGGCCAGTACACACTCATGAAGAAACACAGGAGTAGC	420
Ds	34743	TTTGGTCTACTCTATCAGAGGCCAGTACACACTCATGAAGAAACACAGGAGTAGC	34802
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QY	481	TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTCTTCTTCTCTCTCTCTCC	540
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QY	661	AACATAGGATGAAGTAAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTTCAGAGAGTT	720
Ds	35043	AACATAGGATGAAGTAAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTTCAGAGAGTT	35102
QY	721	AGATTATTTATATATATATATATATAATAATAATAATAATAATAATAATAATAATA	780
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QY	781	TGTGTGTGTATGCTGT	840
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QY	1021	CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAAGC	1080
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QY	1141	CCCCGAGTGGAGAGGTTGCAGCAGGCTCAAGGCGATAGTTCATTCAGCCAACT	1200
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LOCUS			linear PRI 30-APR-1996

Human coagulation factor IX gene; complete cds.

K02402.1 GI:182612

Alu repeat; Christmas factor; KpnI repetitive sequence;

antihemophilic factor B; factor IX; repeat region; simple

repetitive sequence.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 38059)

Yoshitake,S., Schach,B.G., Foster,D.C., Davie,E.W. and Kurachi,K.

Nucleotide sequence of the gene for human factor IX (antihemophilic

factor B)

Biochemistry 24 (14), 3736-3750 (1985)

86000558

2994716

2 (bases 23487 to 23556)

Rees,D.J., Rizza,C.R. and Brownlee,G.G.

Haemophilia B caused by a point mutation in a donor splice junction

of the human factor IX gene

Nature 316 (6029), 643-645 (1985)

85296286

4033760

3 (bases 23378 to 23387)

Graham,J.B., Ljahn,D.B., Lord,S.T., Kirshstein,J., Nilsson,I.M.,

Wallmark,A., Ljung,R., Frazier,L.D., Ware,J.L., Lin,S.W.,

Stafford,D.W. and Bosco,J.

The Maimo polymorphism of coagulation factor IX, an immunologic

polymorphism due to dimorphism of residue 148 that is in linkage

disequilibrium with two other F.IX polymorphisms

Am. J. Hum. Genet. 42 (4), 573-580 (1988)

88161064

2450455

4 (sites)

Hirosawa,S., Fahner,J.B., Salier,J.-P., Wu,C.-T., Lovrien,E. and

Kurachi,K.

Structural and functional basis of the developmental regulation of

human factor IX gene: factor IX Leyden

Unpublished (1990)

Original source text: Homo sapiens (clone:

FIX-lambda-[6,36,53,61].) (tissue library: T.Maniatis et al.) DNA;

and Homo sapiens (clone: FIX-lambda-4243) DNA.

Sequence for [1] kindly submitted on floppy by K.Kurachi,

05-AUG-1985.

[1] notes a potential TATA box (2939-2942) and polyadenylation

signal (35701-35706); and notes two start codons (downstream of the

start codon annotated below) that may be alternative and/or

preferred starts for the factor IX prepropeptide. Several tracts

of simple repetitive sequence are present [1], including regions

with the potential for hairpin and/or Z-DNA formation. [1]

describes six long open reading frames in the intron and on the

complementary strand.

Location/Qualifiers

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DEFINITION Sequence 83 from patent US 6610906.
ACCESSION AR390828
VERSION AR390828.1 GI:40113179
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1272)
AUTHORS Kurachi,K. and Kurachi,S.
TITLE Nucleotide sequences for gene regulation and methods of use thereof
JOURNAL Patent: US 6610906-A 83 26-AUG-2003;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 12:54:08 ; Search time 208 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1273	100.0	38059	4	US-09-328-925-4
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6	1271.4	99.9	1273	4	US-09-328-925-76
7	1271.4	99.9	1273	4	US-09-328-925-77
8	1271.4	99.9	2833	4	US-09-328-925-52
9	1271.4	99.9	36755	4	US-09-949-016-16994
10	1269.8	99.7	1273	4	US-09-328-925-78
11	1269.8	99.7	2792	4	US-09-118-748-1
12	1269.8	99.7	2802	3	US-08-742-877-1
13	1266.6	99.5	1273	4	US-09-328-925-79
14	1261	99.1	1272	4	US-09-328-925-82
15	1261	99.1	1275	4	US-09-328-925-80
16	1260	99.0	1276	4	US-09-328-925-81
17	1186.4	93.2	2340	3	US-08-742-877-3
18	110	8.6	1610	1	US-08-209-846A-6
19	110	8.6	1610	2	US-08-472-809B-6
20	110	8.6	1610	3	US-08-438-265-6
21	109	8.6	1548	1	US-08-106-078-15
22	109	8.6	1548	1	US-08-591-492-21
23	109	8.6	1548	2	US-08-484-891-6
24	109	8.6	1548	4	US-09-150-811-6
25	89	7.0	101	4	US-09-328-925-58
26	64	5.0	7218	1	US-08-232-463-14
27	63.4	5.0	601	4	US-09-949-016-23918

ALIGNMENTS

RESULT 1

US-09-328-925-3
; Sequence 3, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-925-3

Query Match	100.0%	Score 1273	DB 4	Length 1273
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1273	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTGTAGATTGGAATATATACATTCTAT	60	Sequence 148605
Db	1	GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTGTAGATTGGAATATATACATTCTAT	60	Sequence 23913, A
Qy	61	GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTTTACATTTTACCTGAGCAAAATTCATT	120	Sequence 148600
Db	61	GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTTTACATTTTACCTGAGCAAAATTCATT	120	Sequence 23914, A
Qy	121	GAATATGGAACCACTAGAGGAATAATGTGTAGGAATTTACAGTCATTCTTAAGGGCC	180	Sequence 23915, A
Db	121	GAATATGGAACCACTAGAGGAATAATGTGTAGGAATTTACAGTCATTCTTAAGGGCC	180	Sequence 23916, A
Qy	181	CAGCCCTTGACAAAATTTGGAAGTTAAATTTCCACTCTGTCCATCAGATCTATGGTTC	240	Sequence 23917, A
Db	181	CAGCCCTTGACAAAATTTGGAAGTTAAATTTCCACTCTGTCCATCAGATCTATGGTTC	240	Sequence 23919, A
Qy	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCATTCCTCCGAT	300	Sequence 23920, A
Db	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCATTCCTCCGAT	300	Sequence 23921, A
Qy	301	CTTCTTTTGTCTTCCAAACCAAAACATCAATGTTTATAGTTCTGTATACAGTACAGGATC	360	Sequence 23922, A
Db	301	CTTCTTTTGTCTTCCAAACCAAAACATCAATGTTTATAGTTCTGTATACAGTACAGGATC	360	Sequence 23923, A
Qy	361	TTTGTGTACTCTATCAACAAGGCCAGTACCACTCATGAAGAAACACAGGAGTAGC	420	Sequence 148601
Db	361	TTTGTGTACTCTATCAACAAGGCCAGTACCACTCATGAAGAAACACAGGAGTAGC	420	Sequence 148602
				Sequence 148603
				Sequence 148604
				Sequence 148606

[illegible]

RESULT 2

US-09-053-871A-22

; Sequence 22, Application US/09053871A

; Patent No. 6315995

; GENERAL INFORMATION:

; APPLICANT: Pinsky, David J.
: APPLICANT: Stern, David

;
: APPLICANT: Stern, David
: APPLICANT: Rose, Eric

APPLICANT: ROBE, ERIC
APPLICANT: Solomon, Rob

APPLICANT: Schmidt, Ann Marie

Qy	841	AGCCATTCTAAGAGCTTGTATGGTATTATGGAGGTCTGACTAGGCAATGATTTTCAAGAGGCA	900
Db	2275	AGCCATTCTAAGAGCTTGTATGGTATTATGGAGGTCTGACTAGGCAATGATTTTCAAGAGGCA	2334
Qy	901	AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTTGACCCAGACATATTTGTACTCTTT	960
Db	2335	AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTTGACCCAGACATATTTGTACTCTTT	2394
Qy	961	CTAAAAATAATAATAATGCTTAACAGAAAGAGAGAACCGTTTCGTTTGCATATCTACAG	1020
Db	2395	CTAAAAATAATAATAATGCTTAACAGAAAGAGAGAACCGTTTCGTTTGCATATCTACAG	2454
Qy	1021	CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTCTTCCAGCAGTGTTCAGAGCCCAAGC	1080
Db	2455	CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTCTTCCAGCAGTGTTCAGAGCCCAAGC	2514
Qy	1081	AAGAAGTTGAAGTTGCCTTAGACACAGAGACATAAGTATCATGTCTCTTAACTAGCATA	1140
Db	2515	AAGAAGTTGAAGTTGCCTTAGACACAGAGACATAAGTATCATGTCTCTTAACTAGCATA	2574
Qy	1141	CCCCGAAGTGGAGAAGGCTGAGCAGGCTCAAAGGCATAAGTCATTTCCAATCAGCCAACT	1200
Db	2575	CCCCGAAGTGGAGAAGGCTGAGCAGGCTCAAAGGCATAAGTCATTTCCAATCAGCCAACT	2634
Qy	1201	AAGTTGCTCTTTCTCGTTTCGTTTCCAGTGTTCACCATGGAAACATTTGATTAATAGTTTTC	1260
Db	2635	AAGTTGCTCTTTCTCGTTTCGTTTCCAGTGTTCACCATGGAAACATTTGATTAATAGTTTTC	2694
Qy	1261	TATCTTGAATCTT 1273	
Db	2695	TATCTTGAATCTT 2707	
RESULT 3			
US-10-133-907-2			
; Sequence 2, Application US/10133907			
; Patent No. 667369			
; GENERAL INFORMATION:			
; APPLICANT: Chien, Kenneth R			
; APPLICANT: Hoshijima, Masahiko			
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of F			
; TITLE OF INVENTION: with vesicle vector			
; FILE REFERENCE: 6627-Pall170			
; CURRENT APPLICATION NUMBER: US/10/133,907			
; CURRENT FILING DATE: 2002-04-25			
; PRIOR APPLICATION NUMBER: 60/286,314			
; PRIOR FILING DATE: 2001-04-25			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 2			
; LENGTH: 2804			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-133-907-2			
Query Match 100.0%; Score 1273; DB 4; Length 2804;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GGCTCTCACTAACTAATCACTTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT	60
Db	1464	GGCTCTCACTAACTAATCACTTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT	1523
Qy	61	GATCATTTGCTTTTCTCTTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTGATTA	120
Db	1524	GATCATTTGCTTTTCTCTTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTGATTA	1583
Qy	121	GAAATGGAAACCACTAGAGGAATAATATGTTTAGGAAATTCAGTCATTTCTAAGGGCC	180
Db	1584	GAAATGGAAACCACTAGAGGAATAATATGTTTAGGAAATTCAGTCATTTCTAAGGGCC	1643
Qy	181	CAGCCCTTGACAAATTTGTGAAGTTAAATTTCTCCACTCTCTCCATCAGACTATGGTTC	240

Db	1644	CAGCCCTTGACAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC	1703
Qy	241	TCCACTATGGCAACTAACTCACTCAATTTTTTCCCTCCTTTAGCAGCATTTCCCATCTTCCCGAT	300
Db	1704	TCCACTATGGCAACTAACTCACTCAATTTTTTCCCTCCTTTAGCAGCATTTCCATCTTCCCGAT	1763
Qy	301	CTTCTTTGCTTCTCCAAACCAAAACATCAATTGTTTATTAGTTCTGTATACAGTACAGGATC	360
Db	1764	CTTCTTTGCTTCTCCAAACCAAAACATCAATTGTTTATTAGTTCTGTATACAGTACAGGATC	1823
Qy	361	TTTGGTCTACTCTATCACAAAGGCAGTACACACTCATGAAGAAGAACACACAGAGTAGC	420
Db	1824	TTTGGTCTACTCTATCACAAAGGCAGTACACACTCATGAAGAAGAACACAGAGTAGC	1883
Qy	421	TGAGAGCTAAAACTCATCAAAAACACTACTCTCTTTTCTCTCTACTACCTTATTCTCTCAATCTT	480
Db	1884	TGAGAGCTAAAACTCATCAAAAACACTACTCTCTTTTCTCTCTACTACCTTATTCTCTCAATCTT	1943
Qy	481	TTACCTTTTCCAAATCCCAATCCCAATCCAGTTTTTCTTTCTTTCTTACTCTCTCTCTCCC	540
Db	1944	TTACCTTTTCCAAATCCCAATCCCAATCCAGTTTTTCTTTCTTTACTCTCTCTCTCCC	2003
Qy	541	TTTTTACCCTCCATGGTGGTTTAAAGGAGAGATGGGAGCATCATTCGTGTATATCTTCTGTAT	600
Db	2004	TTTTTACCCTCCATGGTGGTTTAAAGGAGAGATGGGAGCATCATTCGTGTATATCTTCTGTAT	2063
Qy	601	CACAGTTATACATGTCTATCAAAACCCAGACTCTCTTCCATAGTGGAGACTTGTCTTTTCAG	660
Db	2064	CACAGTTATACATGTCTATCAAAACCCAGACTCTCTTCCATAGTGGAGACTTGTCTTTTCAG	2123
Qy	661	AACATAGGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTT	720
Db	2124	AACATAGGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTT	2183
Qy	721	AAGTTATTTATATATATAATATATATATAATAATATATAATATATAATAATAATATATATAG	780
Db	2184	AAGTTATTTATATATATAATATATATAATAATAATATATAATAATAATAATAATAATATATAG	2243
Qy	781	TGTGTGTGTATGTGCGTGTGTGTAGACACACACGCAATACACATATAATATGGGAAGCAATA	840
Db	2244	TGTGTGTGTATGTGCGTGTGTGTAGACACACACGCAATACACATATAATATGGGAAGCAATA	2303
Qy	841	AGCCATTTCTAAGAGCTTGTATGGTTATGGAGTCTGACTAGGCATGATTTTTCAGAAAGGCA	900
Db	2304	AGCCATTTCTAAGAGCTTGTATGGTTATGGAGTCTGACTAGGCATGATTTTTCAGAAAGGCA	2363
Qy	901	AGATTGGCATATCATTTGTAACTAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT	960
Db	2364	AGATTGGCATATCATTTGTAACTAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT	2423
Qy	961	CTAAAAATATAATAATATGCTAACAGAAAGAGAGAACCGTTCGTTTGCATCTACAG	1020
Db	2424	CTAAAAATATAATAATATGCTAACAGAAAGAGAGAACCGTTCGTTTGCATCTACAG	2483
Qy	1021	CTAGTAGAGACTTTGAGGAAGAAATTCAAAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAAGC	1080
Db	2484	CTAGTAGAGACTTTGAGGAAGAAATTCAAAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAAGC	2543
Qy	1081	AAGAAGTTGAAGTTGCTGTAGACAGAGGACATAAGTATCATGTCTCTTTTAACTAGCATA	1140
Db	2544	AAGAAGTTGAAGTTGCTGTAGACAGGAGCATAAAGTATCATGTCTCTTTTAACTAGCATA	2603
Qy	1141	CCCCGAAGTGGAGAAAGGGTGCAGCAGGCTCAAGGCATAAGTTCATTTCCATCAGCCAACT	1200
Db	2604	CCCCGAAGTGGAGAAAGGGTGCAGCAGGCTCAAGGCATAAGTTCATTTCCATCAGCCAACT	2663
Qy	1201	AAGTTGTCTTTTCTCGTGTTCGTGTTTTCACCATGGAACTATTTGATTTATAGTTTAACTCTTC	1260
Db	2664	AAGTTGTCTTTTCTCGTGTTCGTGTTTTCACCATGGAACTATTTGATTTATAGTTTAACTCTTC	2723
Qy	1261	TATCTTGAATCTTT	1273
Db	2724	TATCTTGAATCTTT	2736

Db 61 ATCATTTGCTTTTCTCTTTTACAGGGGAGAAATTTTATATTTTACCTGAGCAAAATTTGATTTAG 120
QY 122 AAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTTACAGTCAATTTCTTAAGGGCCC 181
Db 121 AAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTTACAGTCAATTTCTTAAGGGCCC 180
QY 182 AGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCAGTCTGTCCATCAGATACACTATGTTTCT 241
Db 181 AGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCAGTCTGTCCATCAGATACACTATGTTTCT 240
QY 242 CCACTATGGCAACTACTCACTCAATTTTCCCTTCTTAGCAGCATTTCCATCTTCCCGATC 301
Db 241 CCACTATGGCAACTACTCACTCAATTTTCCCTTCTTAGCAGCATTTCCATCTTCCCGATC 300
QY 302 TTCTTTGCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCT 361
Db 301 TTCTTTGCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCT 360
QY 362 TTGGTCTACTCTATACAGGCCAGTACCACTCATGATGAAGAAAGAACACAGAGTAGCT 421
Db 361 TTGGTCTACTCTATACAGGCCAGTACCACTCATGAAGAAAGAACACAGAGTAGCT 420
QY 422 GAGAGGCTAAACTCATCAAAACACTACTCTCTTTTCCCTCTACCTTATTCCTCAATCTTT 481
Db 421 GAGAGGCTAAACTCATCAAAACACTACTCTCTTTTCCCTCTACCTTATTCCTCAATCTTT 480
QY 482 TACCTTTTCCAAATCCCAATCCCAATCAGTTTCTTCTTCTTACTCCCTCTCTCCCT 541
Db 481 TACCTTTTCCAAATCCCAATCCCAATCAGTTTCTTCTTCTTACTCCCTCTCTCCCT 540
QY 542 TTTACCTCTCATCGTCTTAAAGGAGAGTGGGAGCATCATCTGTATATATATAGT 601
Db 541 TTTACCTCTCATCGTCTTAAAGGAGAGTGGGAGCATCATCTGTATATATATAGT 600
QY 602 ACAGTTATATATCTCTATCAAAACCACTCTGTTTCCATAGTGGAGACTTGTCTTTTTCAGA 661
Db 601 ACAGTTATATATCTCTATCAAAACCACTCTGTTTCCATAGTGGAGACTTGTCTTTTTCAGA 660
QY 662 ACATAGGGATGAAGTGAAGTCTGAAAGTGTGGGGGAAAGTGTCTTTTCAGAGAGTTA 721
Db 661 ACATAGGGATGAAGTGAAGTCTGAAAGTGTGGGGGAAAGTGTCTTTTCAGAGAGTTA 720
QY 722 AGTTATTTTATATATATATATATATAATAATATATATATATATATATATATAGT 781
Db 721 AGTTATTTTATATATATATATATATAATAATATATATATATATATATATATAGT 780
QY 782 GTGTGTGTATCGTGTGTGTAGACACACACGATACACACATATAATGGAAGCAATAA 841
Db 781 GTGTGTGTATCGTGTGTGTAGACACACACGATACACACATATAATGGAAGCAATAA 840
QY 842 GCCATTTAAGAGCTTGTATGTTATGAGGCTGTGATAGGATGATTTTACGAGGCAAA 901
Db 841 GCCATTTAAGAGCTTGTATGTTATGAGGCTGTGATAGGATGATTTTACGAGGCAAA 900
QY 902 GATTTGCATATCATTTGTAATAAAAAAGCTGACATTTGACCCAGACATATTTGTAATCTTTTC 961
Db 901 GATTTGCATATCATTTGTAATAAAAAAGCTGACATTTGACCCAGACATATTTGTAATCTTTTC 960
QY 962 TAAAAATATAATAATGCTTAACAGAAAGAGAAACCGTTTCGTTTGCATCTACAGC 1021
Db 961 TAAAAATATAATAATGCTTAACAGAAAGAGAAACCGTTTCGTTTGCATCTACAGC 1020
QY 1022 TAGTAGAGACTTTGAGGAAGAATTTCAACAGTGTCTTTCAGCAGTGTCTTTCAGAGCCCAAGCA 1081
Db 1021 TAGTAGAGACTTTGAGGAAGAATTTCAACAGTGTCTTTCAGCAGTGTCTTTCAGAGCCCAAGCA 1080
QY 1082 AGAAGTTGAAGTTGCCCTAGACAGAGGACATAGTATCATGTCTCCCTTTAACTTAGCATAC 1141
Db 1081 AGAAGTTGAAGTTGCCCTAGACAGAGGACATAGTATCATGTCTCTCTTTAACTTAGCATAC 1140
QY 1142 CCCGAAGTGGAGGGTGCAGAGGCTCAAGGCAATAGTCAATTCCTCAATCAGCCAACTA 1201

Db 1141 CCCGAAGTGGAGGGTGCAGAGGCTCAAGGCAATAGTCAATTCCTCAATCAGCCAACTA 1200
QY 1202 AGTTGTCTCTTTTCTGTTTCTGTTTCCATGGAACATTTTGTATTAGTTAATCTCTTCT 1261
Db 1201 AGTTGTCTCTTTTCTGTTTCTGTTTCCATGGAACATTTTGTATTAGTTAATCTCTTCT 1260
QY 1262 ATCTTGAATCTT 1273
Db 1261 ATCTTGAATCTT 1272

RESULT 6
US-09-328-925-76
; Sequence 76, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 76
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-328-925-76

Query Match 99.9%; Score 1271.4; DB 4; Length 1273;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTGGTAGATTGAAATATATATATATAT 60
Db 1 GGCCTCTGACTAACTAACTCACTTTCCCATCTTTTGGTAGATTGAAATATATATATATAT 60
QY 61 GATCATTTGCTTTTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTTGATTA 120
Db 61 GATCATTTGCTTTTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTTGATTA 120
QY 121 GAAATGGAACCACTAGAGGAATAATGTTTGGTAGAAATTTACAGTCAATTTCTTAAGGGCC 180
Db 121 GAAATGGAACCACTAGAGGAATAATGTTTGGTAGAAATTTACAGTCAATTTCTTAAGGGCC 180
QY 181 CAGCCCTTGACAAAAATTTGAAAGTTTAAATTTCCCATCTGTCTCCATCAGATATCTATGTTTC 240
Db 181 CAGCCCTTGACAAAAATTTGAAAGTTTAAATTTCCCATCTGTCTCCATCAGATATCTATGTTTC 240
QY 241 TCCATATGCGAACTAACTCACTCAATTTTCCCTCTTACAGAGCAATTTCCATCTTCCCGAT 300
Db 241 TCCATATGCGAACTAACTCACTCAATTTTCCCTCTTACAGAGCAATTTCCATCTTCCCGAT 300
QY 301 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATAGTTTCTGTATACAGTACAGATC 360
Db 301 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATAGTTTCTGTATACAGTACAGATC 360
QY 361 TTTTGTGTACTCTATCACAAGGCCAGTACCACTCATGAAGAAAGAACACAGGAGTAGC 420
Db 361 TTTTGTGTACTCTATCACAAGGCCAGTACCACTCATGAAGAAAGAACACAGGAGTAGC 420
QY 421 TCAGAGGCTTAAACTCATCAAAAAACACTACTCTCTTTTCCCTCTACCGTATTTCTCAATCTT 480
Db 421 TCAGAGGCTTAAACTCATCAAAAAACACTACTCTCTTTTCCCTCTACCGTATTTCTCAATCTT 480
QY 481 TTTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTTCTTCTTCTTCTTCTTCTTCTCTCC 540
Db 481 TTTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTTCTTCTTCTTCTTCTTCTTCTCTCC 540

Qy	541	TTTTACCCCTCATCGTCTGTTAAAGAGAGATGGGGAGCATCAITTCCTGTTATACITCTGTGA	600
Db	541	TTTTACCCCTCATCGTCTGTTAAAGAGAGATGGGGAGCATCAITTCCTGTTATACITCTGTGA	600
Qy	601	CACAGTTATACATGCTCTATCAAAACCCAGACITTCCTCCATAGTGGAGACITTCGTTTTTCAG	660
Db	601	CACAGTTATACATGCTCTATCAAAACCCAGACITTCCTCCATAGTGGAGACITTCGTTTTTCAG	660
Qy	661	AACATAGGGATGAAGTAGTGCCTGAAAAAGTTTTGGGGGAAAAAGTTTCCTTCAGAGAGTT	720
Db	661	AACATAGGGATGAAGTAGTGCCTGAAAAAGTTTTGGGGGAAAAAGTTTCCTTCAGAGAGTT	720
Qy	721	AAGTTATTTTATATATATATATATATATAAAATATATAAATATATAAATATATATATAG	780
Db	721	AAGTTATTTTATATATATATATATATAAAATATATAAATATATAAATATATATATAG	780
Qy	781	TGTCGTGTGTATCGGTGTGTAGACACACACCCATACACACATATAAATGGGANGCAATA	840
Db	781	TGTCGTGTGTATCGGTGTGTAGACACACACCCATACACACATATAAATGGGANGCAATA	840
Qy	841	AGCCATCTTAAGAGCTTGTATGGTTATGGAGGCTCTGACTAGGCATGATTTTCACGAAGGCA	900
Db	841	AGCCATCTTAAGAGCTTGTATGGTTATGGAGGCTCTGACTAGGCATGATTTTCACGAAGGCA	900
Qy	901	AGATTGGCATATCAITTTGTAACCTAAAAAGCTGACATTCAGCCAGACATATTTGTACTCTTT	960
Db	901	AGATTGGCATATCAITTTGTAACCTAAAAAGCTGACATTCAGCCAGACATATTTGTACTCTTT	960
Qy	961	CTAAAAATAATAATAAATGCTTAACAGAAAGAGAGAACCGTTTCGTTTGCATCTACAG	1020
Db	961	CTAAAAATAATAATAAATGCTTAACAGAAAGAGAGAACCGTTTCGTTTGCATCTACAG	1020
Qy	1021	CTAGTAGAGACTTTTGAGGAAGAAATTCACACAGTGTCTTCAGCAGTGTTCAGAGCCCAAGC	1080
Db	1021	CTAGTAGAGACTTTTGAGGAAGAAATTCACACAGTGTCTTCAGCAGTGTTCAGAGCCCAAGC	1080
Qy	1081	AAGAAGTTGAAGTTTGCCTAGACACAGAGACATAAGTATCATGTCTCTTTAACTAGACATA	1140
Db	1081	AAGAAGTTGAAGTTTGCCTAGACACAGAGACATAAGTATCATGTCTCTTTAACTAGACATA	1140
Qy	1141	CCCCGAAGTGGAGAGGGTCAGCAGGCTCAAGGCATTAAGTCATTCCAATCAGCCCAACT	1200
Db	1141	CCCCGAAGTGGAGAGGGTCAGCAGGCTCAAGGCATTAAGTCATTCCAATCAGCCCAACT	1200
Qy	1201	AAGTTGTCTTTTCTGTTTTCGTTTCACCATGGAAATTTGATTATAGTTAATCTCTTC	1260
Db	1201	AAGTTGTCTTTTCTGTTTTCGTTTCACCATGGAAATTTGATTATAGTTAATCTCTTC	1260
Qy	1261	TATCTTGAATCTTT	1273
Db	1261	TATCTTGAATCTTT	1273

RESULT 7

US-09-328-925-77
Sequence 77, Application US/09328925
Patent No. 6610906
GENERAL INFORMATION:
APPLICANT: Kurachi, Kotoku
APPLICANT: Kurachi, Sumiko
TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: UM-03603
CURRENT APPLICATION NUMBER: US/09/328,925
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 77
LENGTH: 1273
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic


```
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16994
; LENGTH: 36755
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16994

Query Match          99.9%; Score 1271.4; DB 4; Length 36755;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCTCTCACTAACTACATTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT 60
DB 33414 GGCCTCTCACTAACTACATTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT 33473

QY 61 GATCATTTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA 120
DB 33474 GATCATTTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA 33533

QY 121 GAAATGGAAACCACTAGAGGAATATAATGTGTAGGAATATACAGTCATTTCTAAGGGCC 180
DB 33534 GAAATGGAAACCACTAGAGGAATATAATGTGTAGGAATATACAGTCATTTCTAAGGGCC 33593

QY 181 CAGCCCTTGACAAAATTTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATACATATGGTTTC 240
DB 33594 CAGCCCTTGACAAAATTTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATACATATGGTTTC 33653

QY 241 TCACATATGGCAACTAACTCACTCAATTTTCCCTCTTAGCAGCATTCCTCCCAT 300
DB 33654 TCACATATGGCAACTAACTCACTCAATTTTCCCTCTTAGCAGCATTCCTCCCAT 33713

QY 301 CTTCTTTGCTCTCCCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
DB 33714 CTTCTTTGCTCTCCCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 33773

QY 361 TTTTGGTCTACTCTATCACAAGGCCAGTACACACTCATGAAGAAAGAACACAGGAGTAGC 420
DB 33774 TTTTGGTCTACTCTATCACAAGGCCAGTACACACTCATGAAGAAAGAACACAGGAGTAGC 33833

QY 421 TGAGAGGCTTAAACTCATCAAAAACACTACTCTTTTCTCTACCCCTATCTCTCAATCTT 480
DB 33834 TGAGAGGCTTAAACTCATCAAAAACACTACTCTTTTCTCTACCCCTATCTCTCAATCTT 33893

QY 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTCTTCTTACTCCCTCTCTCC 540
DB 33894 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTCTTCTTACTCCCTCTCTCC 33953

QY 541 TTTTACCCCTCCATGGTCGTTAAAGGAGAGATGGGAGCATCATTTCTGTTATATCTCTGTA 600
DB 33954 TTTTACCCCTCCATGGTCGTTAAAGGAGAGATGGGAGCATCATTTCTGTTATATCTCTGTA 34013

QY 601 CACAGTTATACATGCTTATCAAAACCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTTCAG 660
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QY 661 AACATAGGATGAAGTAAAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTTTCAGAGATT 720
DB 34074 AACATAGGATGAAGTAAAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTTTCAGAGATT 34133

QY 721 AAGTTATTTTATATATATATATATATAATAATATATATAACAATATAATATATATAG 780
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DB 34134 AAGTTATTTTATATATATATATATAATAATAATAATAATAATAATAATAATATATAG 34193
QY 781 TGTGTGTGTATGCGTGTGTGTAGACACACACGACATACACACATATATATATGAAGCAATA 840
DB 34194 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGACATACACACATATATATGAAGCAATA 34253
QY 841 AGCCATTTCTAAGAGCTTGTATGGTGTATGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900
DB 34254 AGCCATTTCTAAGAGCTTGTATGGTGTATGAGGTCTGACTAGGCATGATTTCACGAAGGCA 34313
QY 901 AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT 960
DB 34314 AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT 34373
QY 961 CTAAAAATAATAATAATAATGCTAAACAGAAAGAGAACCGTTTCGTTTGCATCTACAG 1020
DB 34374 CTAAAAATAATAATAATAATGCTAAACAGAAAGAGAACCGTTTCGTTTGCATCTACAG 34433
QY 1021 CTAGTAGAGACTTTTGAGGAGAAATTTCAACAGTGTCTTTCAGCAGTGTTCAGAGCCAAAGC 1080
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DB 34494 AAGAAAGTTGAAGTTCCCTAGACGAGACATAAGTATCATGTCTCTCTTTAACTAGCATATA 34553
QY 1141 CCCCAGAGTGAGAAAGGTGCGAGAGGCTCAAGGCGATAAGTCATTCCAATCAGGCCAACT 1200
DB 34554 CCCCAGAGTGAGAAAGGTGCGAGAGGCTCAAGGCGATAAGTCATTCCAATCAGGCCAACT 34613
QY 1201 AAGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGTATTAGTTAATCCCTTC 1260
DB 34614 AAGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGTATTAGTTAATCCCTTC 34673
QY 1261 TATCTTGAATCTT 1273
DB 34674 TATCTTGAATCTT 34686
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RESULT 10

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US-09-328-925-78
; Sequence 78, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-328-925-78
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Query Match          99.7%; Score 1269.8; DB 4; Length 1273;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 61 GATCATTTGCTTTTCTTTTACAGGGGAGAAATTTCATATTTTACCTGAGCAAAATTGATTA 120
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QY 241 TCCACTATGCGCAACTAACTCACTCAATTTTCCCTCTCTTAGCAGCAATTTCCATCTTCCCGAT 300
DB 241 TCCACTATGCGCAACTAACTCACTCAATTTTCCCTCTCTTAGCAGCAATTTCCATCTTCCCGAT 300
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DB 601 CACAGTTATACATGTTCTATCAAAACCCAGACTTCTTCCATAGTGGAGACTTGTCTTTCAG 660
QY 661 AACATAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 720
DB 661 AACATAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 720
QY 721 AAGTTATTTATATATATATATATATATATATATATATATATATATATATATATATATATAG 780
DB 721 AAGTTATTTATATATATATATATATATATATATATATATATATATATATATATATATATAG 780
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DB 781 TGTGTGTGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 841 AGCCATTTAAGAGCTTGTATGTTTATGAGGCTGTGACTAGGATGATTTTCAAGAGGCA 900
DB 841 AGCCATTTAAGAGCTTGTATGTTTATGAGGCTGTGACTAGGATGATTTTCAAGAGGCA 900
QY 901 AGATTGGCATATCATTTGTAACCTTAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT 960
DB 901 AGATTGGCATATCATTTGTAACCTTAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT 960
QY 961 CTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1020
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DB 1081 AAGAAGTTGAAGTTGCTTACAGAGGACATATGATCATGTCTCTCTTTTAACTAGCATTA 1140
QY 1141 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGACATAGTCAATTCCTCAATCAGCAACT 1200
DB 1141 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGACATAGTCAATTCCTCAATCAGCAACT 1200
QY 1201 AAGTTGTCTCTTTTCTGTTTCTGTTTCCACATGGAAACATTTTGAATATATAGTTAACTCTTC 1260
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DB 1201 AAGTTGTCTCTTTTCTGTTTCTGTTTCCGATGGAAACATTTTGAATATATAGTTAACTCTTC 1260
QY 1261 TATCTTTGAATCTTT 1273
DB 1261 TATCTTTGAATCTTT 1273
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RESULT 11

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US-09-118-748-1
; Sequence 1, Application US/09118748A
; Patent No. 6531298
; GENERAL INFORMATION:
; APPLICANT: Stafford, Darrel W.
; APPLICANT: Chang, JinLi
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 5470-183
; CURRENT APPLICATION NUMBER: US/09/118,748A
; EARLIER FILING DATE: 1998-07-17
; EARLIER FILING DATE: 1997-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2792
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence of
; OTHER INFORMATION: human factor IX-R338A
; NAME/KEY: CDS
; LOCATION: (156)..(1400)
US-09-118-748-1
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Query Match 99.7%; Score 1269.8; DB 4; Length 2792;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 1452 GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTGTAGATTGTAATATATACATTTCTAT 1511
QY 61 GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTTTACATTTTACCTGACCAATTCATTA 120
DB 1512 GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTTTACATTTTACCTGACCAATTCATTA 1571
QY 121 GAAAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTAACAGTCAATTTCTAAGGGCC 180
DB 1572 GAAAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTAACAGTCAATTTCTAAGGGCC 1631
QY 181 CAGCCCTTGACAAAATTTGGAAGTTAAATTTCCACTCTGTCCATCAGATATATATGGTTC 240
DB 1632 CAGCCCTTGACAAAATTTGGAAGTTAAATTTCCACTCTGTCCATCAGATATATATGGTTC 1691
QY 241 TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCATTTCCATCTTCCCGAT 300
DB 1692 TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCATTTCCATCTTCCCGAT 1751
QY 301 CTTCTTTTGTCTTCCAAACCAAAACATCAATGTTTATAGTTTCTGTATACAGTACAGGATC 360
DB 1752 CTTCTTTTGTCTTCCAAACCAAAACATCAATGTTTATAGTTTCTGTATACAGTACAGGATC 1811
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DB 1872 TGAGAGGCTTAAACTCATCAAAAACACTACTCTCTTTTCTCTACCTATTTCTCTCAATCTT 1931
QY 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCTCTCTCCC 540
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; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE REFERENCE: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-328-925-80

Query Match 99.1%; Score 1261; DB 4; Length 1275;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1273; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 GGCCCTCCTCACTAATCACTTCCCATCTTTTGTAGATTGAAATATATACATCTAT 60
DB 1 GGCCCTCCTCACTAATCACTTCCCATCTTTTGTAGATTGAAATATATACATCTAT 60

QY 61 GATCATTGCTTTTCTCTTACAGGGAGAAATTCATATTTACCTGAGCAAAATTCATTA 120
DB 61 GATCATTGCTTTTCTCTTACAGGGAGAAATTCATATTTACCTGAGCAAAATTCATTA 120

QY 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATACAGTCATTTCTAAGGGCC 180
DB 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATACAGTCATTTCTAAGGGCC 180

QY 181 CAGCCCTTGACAAAATTTGTAGAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC 240
DB 181 CAGCCCTTGACAAAATTTGTAGAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC 240

QY 241 TCCACTATGGCACTAATCACTCAATTTTCCCTCTTAGCAGCATTCATCTCCCGA- 299
DB 241 TCCACTATGGCACTAATCACTCAATTTTCCCTCTTAGCAGCATTCATCTCCCGAT 300

QY 300 -TCTTCTTTGCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGA 358
DB 301 TTTCTTCTTTGCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGA 360

QY 359 TCTTTGGTCTACTCTATCAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGATTA 418
DB 361 TCTTTGGTCTACTCTATCAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGATTA 420

QY 419 GCTGAGAGGCTAAACCTCATCAAAAACACTACTCTTTTCTCTACCTATTCCTCAATC 478
DB 421 GCTGAGAGGCTAAACCTCATCAAAAACACTACTCTTTTCTCTACCTATTCCTCAATC 480

QY 479 TTTTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTCTTACTCCCTCTCTC 538
DB 481 TTTTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTCTTACTCCCTCTCTC 540

QY 539 CCTTTTACCTCTCATCGTGTAAAGGAGAGATGGGGAGCATCTCTGTATATCTTCG 598
DB 541 CCTTTTACCTCTCATCGTGTAAAGGAGAGATGGGGAGCATCTCTGTATATCTTCG 600

QY 599 TACACAGTTATACATGCTCATCAAAACCCAGCTTGCTTCCATAGTGGAGACTTGTCTTTC 658
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QY 719 TTAAGTTATTTTATATATATATATATATAATAATAATAATAATAATAATAATAATA 778
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DB 779 AGTGTGTGTGTATCGGTGTGTAGACACACAGCATACACATATAATGGAAGCAA 838

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DB 901 CAAGATTGGCATATCATTTGTAATAAAGCTGACATTGACCCAGACATATTGTACTCT 960
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DB 1201 CTAAGTTGTCTCTTTTCTGTTTTCGTTTTCAGCATGGAACATTTTGATTAATCTCT 1260
QY 1259 TCTATCTTGAATCTT 1273
DB 1261 TCTATCTTGAATCTT 1275

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Job time : 212 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gss1.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	527.2	41.4	532	6	CB156936	CB156936 K-EST0215
C 3	456	35.8	515	5	BX414387	BX414387 BX414387
C 4	373	29.3	373	1	AV647038	AV647038 AV647038
C 5	373	29.3	374	1	AV647182	AV647182 AV647182
C 6	299.2	23.5	524	7	CO755183	CO755183 ILLUMIGEN
C 7	273	21.4	385	1	AV656454	AV656454 AV656454
C 8	203	15.9	518	8	AQ456663	AQ456663 HS 5166 A
C 9	149.6	11.8	374	7	CF106639	CF106639 ZP0904D3
C 10	149.6	11.8	688	5	BX926315	BX926315 BX926315
C 11	149.6	11.8	690	5	BX925779	BX925779 BX925779
C 12	147	11.5	257	7	CO755581	CO755581 ILLUMIGEN
C 13	120.6	9.5	583	7	CO740602	CO740602 S1L07a27
C 14	107.4	8.4	592	9	CE730574	CE730574 tigr-gss-
C 15	95.8	7.5	816	6	CA456053	CA456053 AGENCOURT
C 16	86.6	6.8	525	5	BX514685	BX514685 BX514685
C 17	76	6.0	539	1	AA209011	AA209011 mw71n02.1
C 18	73	5.7	507	1	AA270287	AA270287 vb11d10.1
C 19	72.6	5.7	464	5	BP101424	BP101424 BP101424
C 20	68.8	5.4	389	5	BP102450	BP102450 BP102450
C 21	66.2	5.2	400	7	CO701325	CO701325 DG32-1f6
C 22	66.2	5.2	583	5	BP103684	BP103684 BP103684
C 23	63.4	5.0	841	8	AQ782305	AQ782305 HS 3184 B
C 24	62.8	4.9	574	5	BP104057	BP104057 BP104057

C 25	62.2	4.9	1101	9	CNS0039G	AL063921 Drosophila
C 26	60.8	4.8	1029	9	CNS0017V	AL074642 Drosophila
C 27	60.8	4.8	1101	9	CNS0039G	AL063921 Drosophila
C 28	60.2	4.7	468	8	AZ904168	AZ904168 RPCI-24-1
C 29	58.8	4.6	623	6	CD473714	CD473714 rad03-10m
C 30	57.2	4.5	532	8	BH180068	BH180068 016 M 07-
C 31	57.2	4.5	532	9	CNS07MOC	AL617022 T3_end of
C 32	56	4.4	736	9	AG462569	AG462569 Mus muscu
C 33	55.6	4.4	430	2	AW631271	AW631271 hh80d01.y
C 34	54.8	4.3	557	1	AI425351	AI425351 mx89a10.y
C 35	54.8	4.3	684	9	AG091777	AG091777 Pan trogl
C 36	54.6	4.3	469	8	AZ387095	AZ387095 1W0146G20
C 37	54.6	4.3	735	7	CO567891	CO567891 AGENCOURT
C 38	54.4	4.3	522	8	AQ483469	AQ483469 RPCI-11-2
C 39	54.4	4.3	571	7	CN195227	CN195227 TGESty18
C 40	54.2	4.3	722	8	AZ987360	AZ987360 2M0269H23
C 41	54.2	4.3	1101	9	CNS0100X	AL098379 Drosophila
C 42	53.8	4.2	424	8	AQ023352	AQ023352 HS 2179 B
C 43	53.8	4.2	902	9	CNS000CVM	AL060007 Drosophila
C 44	53.6	4.2	753	9	AG294270	AG294270 Mus muscu
C 45	53.4	4.2	680	7	CO567171	CO567171 AGENCOURT

ALIGNMENTS

RESULT 1
BX405727/c
LOCUS BX405727 Homo sapiens FETAL LIVER Homo sapiens CDNA clone
DEFINITION CSODM008Y108 3-PRIME, mRNA sequence.
ACCESSION BX405727
VERSION BX405727.2 GI:46924492
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 943)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30635411.
Contact: Genoscope
Genoscope - Centre National de Séquencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 10715.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSOAM008B04NP16c=10715.f.
Location/Qualifiers
1..943
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODM008Y108"
/tissue type="FETAL LIVER"
/dev stage="fetal"
/clone lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match 61.0%; Score 776.4; DB 5; Length 943;
Best Local Similarity 89.7%; Pred. No. 4.4e-170;

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Db	943	TTGGTCCAAAATCAAGCCAGKCYARACTCATSTRGAGGATCACCGSGKAGCT	884			
Qy	422	GAGAGGCTAAACTCATCAAAACACTACTCTCTTTTCCCTCTACCTTATTCCTCAATCTTT	481			
Db	883	GMVKSCTAAATCTCTY-AAACANTACTCC-TTTACTCTMCCCTATTACAMAATCTTT	826			
Qy	482	TACCTTTTCCAAATCCCAATCCCC-AAATCAGTTTTTCTTTCTTTTACTCCCTCTCTCC	540			
Db	825	NACCATTTCAAAATCMWAATCCCCMAAATCAGTTTTTCTTTCTTTTACTCCCTATCTCC	766			
Qy	541	TTTTACCTCCATGGTCGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATTCTGTA	600			
Db	765	TTTTTACCTCCATSRCTRTTAAAGGAGAGATGGGKMGCATCWTCASTTATATCTTWTGAA	706			
Qy	601	CACAGTTATACATGTCTATCAAAACCCAGACTTCTCTCCATAGTGGAGACTTGCTTTTCAG	660			
Db	705	CACAGWTATACATGTCTATCAAAACCCAACTCKTWMCTTADTGGAAATTTGCTTWMAG	646			
Qy	661	AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGAAAAGTTTCTTTTCAGAGATT	720			
Db	645	AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGAAAAGTCTCTCTCASASWT	586			
Qy	721	AGTTATTTTATATATATATATATATAATAATAATAATAATAATAATAATAATAATA	780			
Db	585	AGWTATTTTATATATATATATATAATAATAATAATAATAATAATAATAATAATA	527			
Qy	781	TGTGTGTGTATGCTGT	840			
Db	526	----NGNTGTTTATGT	471			
Qy	841	AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCAGGAGCA	900			
Db	470	AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCAGGAGCA	411			
Qy	901	AGATTGGCATATCATTTGTAACATAAAAGTGTACATTTGACCCAGACATATTTACTCTTT	960			
Db	410	AGATTGGCATATCATTTGTAACATAAAAGTGTACATTTGACCCABACATATTTACTCTTT	351			
Qy	961	CTAAAAATAATAATAATAATGCTTAACAGAAAGAGAGAACCGTTCGTTTGCATCTACAG	1020			
Db	350	CTAAAAATAATAATAATAATGCTTAACAGAAAGAGAGAACCGTTCGTTTGCATCTACAG	291			
Qy	1021	CTAGTAGACCTTTGAGGAAGAAATCAACAGTGTGTCTTTTCTCAGCAGTGTTCAGAGCCA	1080			
Db	290	CTAGTAGACCTTTGAGGAAGAAATCAACAGTGTGTCTTTTCTCAGCAGTGTTCAGAGCCA	231			
Qy	1081	AGAAGTTGAAGTTGCTAGACAGGACATAGTATCATGTCTCTCTTTTAACTAGCAT	1140			
Db	230	AGAAGTTGAAGTTGCTAGACAGGACATAGTATCATGTCTCTCTTTTAACTAGCAT	171			
Qy	1141	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAGAGGCAATAGTCATTTCCAAATCAGCCA	1200			
Db	170	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAGAGGCAATAGTCATTTCCAAATCAGCCA	111			
Qy	1201	AAGTTGTCTCTTTTCTGGTTTCGTTTACCATGGAAATTTTGAATATAGTTAAATCTTTC	1260			
Db	110	AAGTTGTCTCTTTTCTGGTTTCGTTTACCATGGAAATTTTGAATATAGTTAAATCTTTC	51			
Qy	1261	TATCTTGAATCTT 1273				
Db	50	TATCTTGAATCTT 38				

RESULT 2
CB156936
LOCUS
DEFINITION
K-EST0215940 L17N670205n1 Homo sapiens cDNA clone
L17N670205n1-6-A08 5', mRNA sequence.
ACCESSION
CB156936

VERSION		CB156936.1	GI:28142066
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Mammalia; Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 532) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.	
TITLE		21C Frontier Korean EST Project 2001	
JOURNAL		Unpublished (2002)	
COMMENT		Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 6 Row: A column: 08 High quality sequence stop: 532. Location/Qualifiers 1..532	
FEATURES		source 1..532 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="L17N670205n1-6-A08" /sex="F" /lab_host="Top10F" /clone_lib="L17N670205n1" /note="Organ: Liver; Vector: pT73-Pac; Site 1: EcoRI; Site 2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6 (9): 791-806. RNA was prepared from harvested cell culture."	
ORIGIN		Query Match 41.4%; Score 527.2; DB 6; Length 532; Best Local Similarity 99.4%; Pred. No. 4.9e-112; Matches 529; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Qy	95	CATATTTTACCTGAGCAAAATGATTAGAAAATGGAACCACTAGAGGAATATAATGTGTTA	154
Db	1	CATATTTTACCTGAGCAAAATGATTAGAAAATGGAACCACTAGAGGAATATAATGTGTTA	60
Qy	155	GGAAATTACAGTCATTCTTAAGGGCCAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCC	214
Db	61	GGAAATTACAGTCATTCTTAAGGGCCAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCC	120
Qy	215	ACTGTGTCATCAGATACATATGTTTCTCCACTATGGCAACTAACTCACTCAATTTTCCCT	274
Db	121	ACTGTGTCATCAGATACATATGTTTCTCCACTATGGCAACTAACTCACTCAATTTTCCCT	180
Qy	275	CCTTAGCAGCATTCCTCCGATCTCTTTGCTCTTCCAAACCAACACATCAATGTTT	334
Db	181	CCTTAGCAGCATTCCTCCGATCTCTTTGCTCTTCCAAACCAACATCAATGTTT	240
Qy	335	ATTAGTTCTGTATACAGTACAGGATCTTTGGTGTACTCTATCACAAGGCCAGTACACAC	394
Db	241	ATTAGTTCTGTATACAGTACAGGATCTTTGGTGTACTCTATCACAAGGCCAGTACACAC	300
Qy	395	TCATGAAGAAAGACACAGGAGTAGCTGAGAGGCTTAAAACTCATCAAAAACACTACTCCT	454
Db	301	TCATGAAGAAAGACACAGGAGTAGCTGAGAGGCTTAAAACTCATCAAAAACACTACTCCT	360
Qy	455	TTTCTCTTACCTATTCTCTCAATCTTTTACCTTTTCCAAATCCCAATCCCAAAATCAGTT	514
Db	361	TTTCTCTTACCTATTCTCTCAATCTTTTACCTTTTCCAAATCCCAATCCCAAAATCAGTT	420
Qy	515	TTTCTCTTCTTACTCCCTCTCTCCCTTTTACCCTTCAATGGTTCGTTAAAGGAGAGATGGG	574
Db	421	TTTCTCTTCTTACTCCCTCTCTCCCTTTTACCCTTCAATGGTTCGTTAAAGGAGAGATGGG	480

Db 121 TGACAAAATGTGAAGTAAATTTCTCCACTCTGTCCATCAGATACATATGTTCTCCACTA 180

QY 248 TGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCATCTCCGATCTCTTT 307

Db 181 TGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCATCTCCGATCTCTTT 240

QY 308 GCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGATCTTTGGTC 367

Db 241 GCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGATCTTTGGTC 300

QY 368 TACTCTATCACAGGCCAGTACACACTCATGAAGAAAGAACACAGAGTAGCTGAGAG 427

Db 301 TACTCTATCACAGGCCAGTACACACTCATGAAGAAAGAACACAGAGTAGCTGAGAG 360

QY 428 CTAAAACTCATCA 440

Db 361 CTAAAACTCATCA 373

RESULT 5
AV647182 374 bp mRNA linear EST 15-JAN-2002

LOCUS AV647182 GLC Homo sapiens cDNA clone GLCAVF01 3', mRNA sequence.

ACCESSION AV647182

VERSION AV647182.1 GI:9868196

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 374)

AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

MEDLINE 21625106

PUBMED 11752456

COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Shanghai Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
Source 1..374

/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="GLCAVF01"
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/clone_lib="GLC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 29.3%; Score 373; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.1e-76;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GCTTTTCTCTTACAGGGAGAAATTCATATTTTACCTGACAAATTCATTAGAAATG 127

Db 1 GCTTTTCTCTTACAGGGAGAAATTCATATTTTACCTGACAAATTCATTAGAAATG 60

QY 128 GAACCACTAGAGAAATATATGTTAGGAAATTCAGTCAATTTCTAAGGGCCCGCCCT 187

Db 61 GAACCACTAGAGAAATATATGTTAGGAAATTCAGTCAATTTCTAAGGGCCCGCCCT 120

QY 188 TGACAAAATGTGAAGTAAATTTCTCCACTCTGTCCATCAGATACATATGTTCTCCACTA 247

Db 121 TGACAAAATGTGAAGTAAATTTCTCCACTCTGTCCATCAGATACATATGTTCTCCACTA 180

QY 248 TGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCATCTCCGATCTCTTT 307

Db 181 TGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCATCTCTCCGATCTCTTT 240

QY 308 GCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTC 367

Db 241 GCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTC 300

QY 368 TACTCTATCACAGGCCAGTACACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAG 427

Db 301 TACTCTATCACAGGCCAGTACACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAG 360

QY 428 CTAAAACTCATCA 440

Db 361 CTAAAACTCATCA 373

RESULT 6
CO775183 524 bp mRNA linear EST 04-AUG-2004

LOCUS CO775183

DEFINITION ILLUMIGEN MQ0_52421 Katze MNUV Macaca nemestrina cDNA clone

ACCESSION IBIUM:28458 5' similar to Bases 5 to 424 highly similar to human F9

VERSION CO775183

KEYWORDS (Hs.1330), mRNA sequence.

SOURCE CO775183.1 GI:50976446

ORGANISM EST.

Macaca nemestrina (pig-tailed macaque)

Macaca nemestrina

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae; Macaca.

REFERENCE 1 (bases 1 to 524)

AUTHORS Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.

TITLE Large-scale Rhesus Macaque cDNA Sequencing

JOURNAL Unpublished (2003)

COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.07.21. 661 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see <http://www.macaque.org>

PCR Primers
FORWARD: CCCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGCGGAATTGGGTA
Insert Length: 524 Std Error: 0.00
Place: CL000532 row: F column: 07
Seq primer: CCCTCACTAAAGGGAACAAA
POLYA=Yes.

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Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:9545"
/clone="IBIUM:28458"
/sex="male"
/lab_host="Electromax DH10B"
/clone_lib="Katze MNUV"
/note="Organ: liver; Vector: pDONR 222; Site 1: BsrG I; Site 2: BsrG I; Created from CloneMiner cDNA Library Construction kit (catalog #18249-029)"

ORIGIN


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Query Match      23.5%; Score 299.2; DB 7; Length 524;
Best Local Similarity 94.3%; Pred. No. 6.7e-59;
Matches 332; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 924 AAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTCTAAAAA-TAATAATAATATGC 982
DB 5 AAAAGCTGACATTTGACCGAGATATATTTGACTCTTTCTTAAAAATTAATAATAATATGC 64

QY 983 TAACAGAAAGAGAACCGTTTCGTTTGCATCTACAGCTAGTAGAGACTTTTGGAGGA 1042
DB 65 TAACAGAAAGAGAACAGCTCATTTGCGAGTCTACAACCTAGTAGAGACTTTTGGAGGA 124

QY 1043 ATTCAACAGTGTCTTTCAGCAGTGTTCAGAGCAAGCAAGAGTTGAAGTTCCCTAGAC 1102
DB 125 ATTCAACAGCGTGTCTTTCAGCAGTGTTCAGAGTCAAGAAAGAGTTGAAGTTCCCTAGAC 184

QY 1103 CAGAGGACATAAGTATCATCTCTCTTTAACTAGCATACCCG-GAAGTGAGAGAGGTGC 1161
DB 185 CAGAGGACATAAGTATCATCTCTTTAACTAGCATACCCGTTGAAGTTGAGAGAGGTGC 244

QY 1162 AGCAGGCTCAAGGCAATAGTCAATTCATCAGCCCAACTAAGTTGTCCTTTTCTGGTTTC 1221
DB 245 AGCAGGCTCAAGGCAATAGTCAATTCATCAGCCCAACTAAGTTGTCCTTTTCTGGTTTC 304

QY 1222 GTGTTTCAACATGAACATTTTGAATATAGTATTAATCTTCTATCTTGAATCTT 1273
DB 305 ATGTTTCAACGCGGAACATTTTGAATATAGTATTAATCTTCTATCTTGAATTTT 356
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RESULT 7
AV656454      385 bp  mRNA  linear  EST 16-JAN-2002
LOCUS      AV656454 GLC Homo sapiens cDNA clone GLCERE05 3', mRNA sequence.
DEFINITION      AV656454
ACCESSION      AV656454
VERSION      AV656454.1 GI:9877468
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 385)
AUTHORS      Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE      Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
JOURNAL      21625106
MEDLINE      11752456
PUBMED
COMMENT      Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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source
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/lab_host="SOLR"
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XhoI"
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ORIGIN

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Query Match      21.4%; Score 273; DB 1; Length 385;
Best Local Similarity 86.2%; Pred. No. 8.2e-53;
Matches 337; Conservative 0; Mismatches 0; Indels 54; Gaps 1;

QY 883 CATGATTTCCACGAAGCAAGATTGGCATATCATTTGTAATCTAAAAAGCTGACATTCACCC 942
DB 1 CATGATTTCCAGGAAGCAAGATTGGCATATCATTTGTAATCTAAAAAGCTGACATTCACCC 60

QY 943 AGACATATTTGTACTCTTTCTTAAAAATAATAATAATGCTAAACAGAAAGAGAACCG 1002
DB 61 AGACATATTTGTACTCTT-----

QY 1003 TTCTGTTTGCATCTACAGCTAGTAGAGACTTTTGGAGGAAGAAATTCACAGTGTCTCTTCAG 1062
DB 78 -----TCTACAGCTAGTAGAGACTTTTGGAGGAAGAAATTCACAGTGTCTCTTCAG 126

QY 1063 CAGTGTTCAGAGCCAGCAAGAGTTGAAGTTTGCCTTAGACCAGAGACATAGATATCATG 1122
DB 127 CAGTGTTCAGAGCCAGCAAGAGTTGAAGTTTGCCTTAGACCAGAGACATAGATATCATG 186

QY 1123 TCTCTCTTTAACTAGCATACCCGAGTGGAGAGAGGTGCAGCAGGCTCAAAGGCATAAGT 1182
DB 187 TCTCTCTTTAACTAGCATACCCGAGTGGAGAGAGGTGCAGCAGGCTCAAAGGCATAAGT 246

QY 1183 CATTCCAATCAGCCAACTAAGTTGTCCTTTTCTGGTTTCGTTTCAACATGGAACATTTT 1242
DB 247 CATTCCAATCAGCCAACTAAGTTGTCCTTTTCTGGTTTCGTTTCAACATGGAACATTTT 306

QY 1243 GATTATAGTTAATCTCTTCTATCTTGAATCTT 1273
DB 307 GATTATAGTTAATCTCTTCTATCTTGAATCTT 337
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RESULT 8
AQ456663      518 bp  DNA  linear  GSS 21-APR-1999
LOCUS      HS_5166_A1_C10_T7A RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION      genomic clone Plate=742 Col=19 Row=E, genomic survey sequence.
ACCESSION      AQ456663
VERSION      AQ456663.1 GI:4591998
KEYWORDS      GSS.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 518)
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE      Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL      99380589
MEDLINE      10449764
PUBMED
COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 742 row: E column: 19
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Class: BAC ends
High quality sequence stop: 518.
Location/Qualifiers
1..518
FEATURES
source
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Best Local Similarity 75.8%; Pred. No. 5.1e-24;
Matches 226; Conservative 0; Mismatches 64; Indels 8; Gaps 3;

QY 436 CATCAAAACACACTACTCTCTTCCCTCTACCC-TATTCTCAATCTTTTACCTTTTCCAAA 494
DB 21 CATCAGAAACGCTGCATCTTTCTGGTACCCCTTGGTCTGCATCTGCTATCTTTTCCAAC 80

QY 495 TCCCAATCCCAAAATCAGTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCCTCCATG 554
DB 81 TCCTAACCCCAAGTCAGTTTCT 140

QY 555 GTCTGTTAAAGGAGAGATGGGAGCATCTCTGTATATCTCTGTACACAGTTATACATG 614
DB 141 GGCATTAAAGGAGGAGGAGGAGCATCATCTGTTTACTGCTGTACACAATGATGCAA 200

QY 615 TCTATCAAAACCCAGACTTGTCTCCATAGTG---GAGACTTGTCTTTTCAGAACATAGGGA 670
DB 201 CCTATCAAAACCCAGCTTGTCTTCAATTTGTTCTTGAGCTTGTCTGTATAGCCTGGGA 260

QY 671 TGAAGTAAGTGCTCTGAAAGTTTGGGGAAAAGTTTCTTTTCAGAGAGTTAAGTTATT 728
DB 261 TGAAGTAAGTGCTCTGAA---CTTGGAGGAAAAGTTCTCTTGGAGAGTCACATTATT 315

RESULT 11
LOCUS BX925779
DEFINITION BX925779 Sus Scrofa library (scan) Sus scrofa cDNA clone
ACCESSION scan0021d.o.01 5prim, mRNA sequence.
VERSION BX925779.1 GI:41142627
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 690)
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S.,
Soares,M., Bonaldo,F. and Hatev,F.
TITLE A Pig Normalised Multi-tissue cDNA Library
JOURNAL Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0021 row: 0 column: 1.

FEATURES
source
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ORIGIN

Query Match

11.8%; Score 149.6; DB 5; Length 690;

Best Local Similarity 75.8%; Pred. No. 5.1e-24;
Matches 226; Conservative 0; Mismatches 64; Indels 8; Gaps 3;

QY 436 CATCAAAACACACTACTCTCTTCCCTCTACCC-TATTCTCAATCTTTTACCTTTTCCAAA 494
DB 21 CATCAGAAACGCTGCATCTTTCTGGTACCCCTTGGTCTGCATCTGCTATCTTTTCCAAC 80

QY 495 TCCCAATCCCAAAATCAGTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCCTCCATG 554
DB 81 TCCTAACCCCAAGTCAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 140

QY 555 GTCTGTTAAAGGAGAGATGGGAGCATCTCTGTATATCTCTGTACACAGTTATACATG 614
DB 141 GGCATTAAAGGAGGAGGAGGAGCATCATCTGTTTACTGCTGTACACAATGATGCAA 200

QY 615 TCTATCAAAACCCAGACTTGTCTCCATAGTG---GAGACTTGTCTTTTCAGAACATAGGGA 670
DB 201 CCTATCAAAACCCAGCTTGTCTTCAATTTGTTCTTGAGCTTGTCTGTATAGCCTGGGA 260

QY 671 TGAAGTAAGTGCTCTGAAAGTTTGGGGAAAAGTTTCTTTTCAGAGAGTTAAGTTATT 728
DB 261 TGAAGTAAGTGCTCTGAA---CTTGGAGGAAAAGTTCTCTTGGAGAGTCACATTATT 315

RESULT 12
LOCUS CO775581
DEFINITION CO775581 257 bp mRNA linear EST 04-AUG-2004
IBIUM:29284 5' similar to Bases 5 to 157 highly similar to human F9
(H8.1330), mRNA sequence.
ACCESSION CO775581
VERSION CO775581.1 GI:50976844
KEYWORDS EST.
SOURCE Macaca fascicularis (crab-eating macaque)
ORGANISM Macaca fascicularis
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopithecinæ; Macaca.
1 (bases 1 to 257)
AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.07.29. 411 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org

PCR Primers
FORWARD: CCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGCGAATTGGTA
Insert Length: 257 Std Error: 0.00
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Seq primer: CCTCACTAAAGGGAACAAA
POLYA=Yes.

FEATURES
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/clone_lib="Katze_MFLV"
/note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
Site_2: BsrG I; Created from CloneMiner cDNA Library
Construction kit (catalog #18249-029)"

ORIGIN

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Query Match          11.5%; Score 147; DB 7; Length 257;
Best Local Similarity 93.9%; Pred. No. 1.8e-23;
Matches 153; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 567 GAGATGGGGAGCATCATCTCTGTATATCTCTGTACACAGTTATACATGTCATCAAAACC 626
DB 3 GGGATGGGGAGCATCATCTCTGTATATCTCTGTACGCGAGTTATACATGTCATCAAAACC 62

QY 627 AGACTTGCTTCATAGTGAGACTTCTCTTTCAGAACATAGGATGAAGTGGTCCTG 686
DB 63 AGACTTGCTTTCATAGTGAGACTTCTCTTTCAGAACATAGGATGAAGCAACGTCGCTG 122

QY 687 AAAAGTTTCGGGAAAGTTTCTTTCAGAGAGTTAGTTATTT 729
DB 123 AAAATTTTGGGAAAGTTTCTTTCAGAGAGTTATATATAT 165

RESULT 13
LOCUS CO740602 583 bp mRNA linear EST 29-JUL-2004
DEFINITION SLL07a27j01f1 squirrel liver library 3 Spermophilus lateralis cDNA
ACCESSION CO740602
VERSION CO740602.1 GI:50827872
KEYWORDS EST.
SOURCE Spermophilus lateralis (golden-mantled ground squirrel)
ORGANISM Spermophilus lateralis
REFERENCE 1 (bases 1 to 583)
AUTHORS Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,
Rogers,J. and Cossins,A.R.
TITLE Microarray analysis of transcriptional changes during hibernation
JOURNAL in the golden mantled ground squirrel, Spermophilus lateralis
COMMENT Unpublished (2004)
Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 27 row: j column: 01
Seq primer: Triplex 5'LD (5'-CTCGGAGCGCGCCATTGTGTGGT-3')
High quality sequence stop: 583.
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Site 2: Sfil GGCGGCTCGGC; Normalized cDNA library
prepared from liver of hibernating and summer animals"

ORIGIN
Query Match          9.5%; Score 120.6; DB 7; Length 583;
Best Local Similarity 66.3%; Pred. No. 2.9e-17;
Matches 274; Conservative 0; Mismatches 114; Indels 25; Gaps 6;

QY 861 TGGTTATGAGGTCCTACCTAGGATGATTTTCAGAAAGCAAGATGGCATATCATGTAA 920
DB 120 TGATTATGTCAGTCTGGCTGGGAATGGTTCCATCAAGCAAGGCTG---CAGGTCACTAA 176

Query Match          11.5%; Score 147; DB 7; Length 257;
Best Local Similarity 93.9%; Pred. No. 1.8e-23;
Matches 153; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 921 CTAATAAAGCTGCACATTGACCAGACATATTTGTACTCTTTCTAAATAATAATAATAAT 980
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QY 981 GCTAACAGAAAGAGAACCGTTCGTTTGGCAATCTACAGCTAGTAGAGACTTTGAGGAA 1040
DB 237 AGAA-----AGAACATCCCATTTGCAACCAAGAACTAGCAGATTCTTTAAGGGA 285

QY 1041 GAAATTCACAGTGTCTCTTCAGCAGTGTTCAGAGCCAGCAAGAAGTTGAAGTTGCTTAG 1100
DB 286 GAAATTCACAGCATATCTCCAACATTACCTGGAGTCNAACAA-----GAAGTTTCTTAG 339

QY 1101 ACCAGAGACATAAGTATCATGTCTCTTTAACTAGCATACCCGAAAGTGGAGAGGGTG 1160
DB 340 ACCAGAAACCATGAGCATCATCT---CCTTGGCTAATATATACATCAGTGGAGAGGACA 396

QY 1161 CAGCAGGCTCAAAGGCATCAAGTCAATCCAATCAGCAACTAAGTTGTCTC-TTTTCTGGTT 1219
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QY 1220 TCGTGTTCACCATGCAATTTTGTATTAGTTAATCTCTTCTTCTTGAATCT 1272
DB 456 CCATGTTTCCCAAGGAAGCTTTGTGATTATGATTAACTTTCTTCTTCTACTGAAATTT 508

RESULT 14
LOCUS CE730574 592 bp DNA linear GSS 30-SEP-2003
DEFINITION tigr-gss-dog-17000315417737 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE730574
VERSION CE730574.1 GI:37070694
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 592)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
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Best Local Similarity 68.8%; Pred. No. 3.4e-14;
Matches 181; Conservative 0; Mismatches 71; Indels 11; Gaps 2;

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DB 262 GGTCTCTTACTAACTAATCACTTTT-TTTTATCTCTTTAGATTGACTATATACATCTCT 204

QY 61 GATCATTGCTTTTCTCTTTTACAGGGAGAAT-----TTCATATTTTACCTGAGC 110

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Db 203 GAATACGCTTTTCTCTTTCTGGGAGAAATCTATAGAAATTCCTATTTACTAGACT 144
QY 111 AAATTGATTAGAAAATGGAACTAGAGAAATATAATGTGTAGGAAATACAGTCATT 170
Db 143 AAGTGAATTAGAAAATGTAATCACTACGGAAATGTAAGTGGAACTTTGGACCACT 84
QY 171 TCTAAGGGCCAGCCCTTGACAAAATGTGAAGTTAAATTCCTCACTCTGTCCATCAGAT 230
Db 83 CCACAGGTCTAGCCCTTGGACCAATGTGAGGTAGGTATTCCTCCTGCCGTCAGGT 24
QY 231 ACTATGTTCTCCCACTATGSCAA 253
Db 23 GTTAAGTTTCTCCACTGGGGCAA 1

RESULT 15
CA456053
LOCUS
DEFINITION CA456053 816 bp mRNA linear EST 09-MAR-2004
IMAGE:6745686 5', mRNA sequence.
ACCESSION CA456053
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 816)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Bradfield Laboratory
CDNA Library Preparation: Mark Bittinger
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM00083 row: p column: 05
High quality sequence stop: 564.
Location/Qualifiers

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Site 2: attP1; CDNA made by oligo-dT with attB2 site and
directionally cloned. Priming sequence:
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TTTT-3'. Full-length enriched library was constructed
using the GeneRacer kit by Invitrogen, library
amplification 16 cycles. Library constructed by Mark
Bittinger in the Bradfield laboratory (McArdle Laboratory
for Cancer Research, University of Wisconsin). Note: this
is a NIH_MGC Library."

ORIGIN

Query Match 7.5%; Score 95.8; DB 6; Length 816;
Best Local Similarity 56.7%; Pred. No. 1.8e-11;
Matches 316; Conservative 0; Mismatches 177; Indels 64; Gaps 5;
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QY 83 AGGGGAGAAATTC-----ATATTTTACCTGAGCAAAATGATTAGAAAATGGAAC 131

Db 290 ATAAGCAAGCCCATCTAGGATCTATATTTGTTCTAGAGTAAGTAGGTTAGCAAGTATAAT 349
QY 132 CACTAGAGGAATATAATGTGTGTAGGAAATTTACAGTCATTTCTAAGGGCCAGCCCTTGAC 191
Db 350 CACTAGAGGAATA-----GTTTAGTAGGAGATTCCACCATTTCTGTAAGTCCAGGCCCTTGT 405
QY 192 AAAATTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTCTCCCACTATGGC 251
Db 406 AAAATTAGAAAGTAAAGCTTTCCGTGTGCCCATAGGGCGTGATGGTTCTTTGATACAGAG 465
QY 252 AACTAACTCAGTCNAATTTTCCCTCTTAGCAGCATTCATCTCCCGATCTCTTTGCTTT 311
Db 466 ATGT-----ACCAATTTCCCTCTTGGCAGCAATTCATGTTTAGCTCTTCCCTTGCTA 520
QY 312 CTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTACT 371
Db 521 CTCTCA-----ATTTTATTAGTTTT 540
QY 372 CTATCAAGAGGCCAGTACACACTCATGAAAGAAACACAGAGTAGCTGAGAGGCTAA 431
Db 541 CTATCCAGAAATCTTTAAACCCATTTATGGCCAGAGAATAACAAGAGCAGCTGAAAAAATAA 600
QY 432 AACTCATCAAAAACACTACTCTCTTTTCCCTCTACCCCTATTTCCTCAATCTTTTACCTTTCC 491
Db 601 AACTCATCAAAAAGCATGACTTCTCTCTCT-----GATTTTCTGNAATCTTTGATCTTTTAC 656
QY 492 AAATCCCAATCCCAAAATCAGTTTTTCTCTTTTACTCCCTCTCTCCCTTTTACCCCTCC 551
Db 657 AACTCCCAACCAACAATCACTGAGCCCTCTCCGTCATCTCAGCTTCCCTTTTCTCATC 716
QY 552 ATGGTCGTTTAAAGGAGA 568
Db 717 ACCACTGAAAGAGGAAA 733

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Scoring table: IDENTITY NUC
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Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1273	100.0	2804	16	US-10-133-907-2
5	1273	100.0	2804	21	US-10-956-157-357
6	1273	100.0	2804	21	US-10-804-763-40
7	1273	100.0	38059	9	US-09-880-107-2125

8	1269.8	99.7	2792	9	US-09-118-748-1	Sequence 1, Appli
9	1259	98.9	2773	17	US-10-349-858-16	Sequence 16, Appli
10	1258.6	98.9	2728	21	US-10-741-600-3	Sequence 3, Appli
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13	1258.6	98.9	2831	21	US-10-741-600-4	Sequence 4, Appli
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17	200.6	15.8	201	21	US-10-741-600-2210	Sequence 2210, Ap
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19	200.6	15.8	201	21	US-10-741-600-2779	Sequence 2779, Ap
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21	186	14.6	1438	17	US-10-038-854-5	Sequence 5, Appli
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25	109	8.6	1348	9	US-09-150-811-6	Sequence 6, Appli
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32	51.2	4.0	223556	13	US-10-087-192-394	Sequence 394, App
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35	50.6	4.0	337022	19	US-10-322-696-52	Sequence 52, Appli
36	49.8	3.9	236	19	US-10-674-124A-19594	Sequence 19594, A
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38	49.6	3.9	1207	13	US-10-027-632-203235	Sequence 203235,
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40	49.4	3.9	465	19	US-10-674-124A-19043	Sequence 19043, A
41	49	3.8	352	19	US-10-674-124A-15437	Sequence 15437, A
42	48.8	3.8	606	13	US-10-027-632-227381	Sequence 227381,
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45	48.8	3.8	6692	18	US-10-221-714A-131	Sequence 131, App

ALIGNMENTS

RESULT 1

US-10-956-157-5592
; Sequence 5592, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH:
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE OF INVENTION: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5592
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-5592

Query Match	100.0%	Score 1273;	DB 21;	Length 1400;
Best Local Similarity	100.0%	Pred. No. 1.1e-299;	Mismatches 0;	Indels 0; Gaps 0;
Matches 1273;	Conservative 0;			
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Db 1200 CCCCAGGTGGAGAAAGGGTGCAGAGGCTCAAGGCAATTAAGTCAATCAGGCAACT 1259

Qy 1201 AGTTGTCTCTTTTCTGTTTCCATGGAACATTTTGATTATAGTTAAATCCTTC 1260
Db 1260 AGTTGTCTCTTTTCTGTTTCCATGGAACATTTTGATTATAGTTAAATCCTTC 1319
Qy 1261 TATCTTGAATCTT 1273
Db 1320 TATCTTGAATCTT 1332
RESULT 2
US-09-884-901-7
; Sequence 7, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOPW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1707
; TYPE: DNA
; ORGANISM: HomoSapien
US-09-884-901-7
Query Match 100.0%; Score 1273; DB 9; Length 1707;
Best Local Similarity 100.0%; Pred. No. 1.2e-299; Mismatches 0; Indels 0; Gaps 0;
Matches 1273; Conservative 0;
Qy 1 GGCCTCTCACATACTAATCACTTTCCCATCTTTTGTAGATTGGAATATATACATTTCTAT 60
Db 51 GGCCTCTCACATACTAATCACTTTCCCATCTTTTGTAGATTGGAATATATACATTTCTAT 110
Qy 61 GATCATTTGCTTTTCTCTTTTACAGGGAGAAATTTCAATATTTTACCTGAGCAAAATTGATTA 120
Db 111 GATCATTTGCTTTTCTCTTTTACAGGGAGAAATTTCAATATTTTACCTGAGCAAAATTGATTA 170
Qy 121 GAAATGGAAACCACTAGAGGAATATAATGTGTGTAGGAAATTTACAGTCATTTCTAAGGGCC 180
Db 171 GAAATGGAAACCACTAGAGGAATATAATGTGTGTAGGAAATTTACAGTCATTTCTAAGGGCC 230
Qy 181 CAGCCCTTGACAAAATTTGTAAGTTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC 240
Db 231 CAGCCCTTGACAAAATTTGTAAGTTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC 290
Qy 241 TCACATATGGCAATCACTCAATTTTCCCTCTTACGAGCAATTCATCTTCCCGAT 300
Db 291 TCACATATGGCAATCACTCAATTTTCCCTCTTACGAGCAATTCATCTTCCCGAT 350
Qy 301 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATTAGTTCGTATACAGTACAGGATC 360
Db 351 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATTAGTTCGTATACAGTACAGGATC 410
Qy 361 TTTGCTTACTCTATCACAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTAGC 420
Db 411 TTTGCTTACTCTATCACAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTAGC 470
Qy 421 TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTTCCCTCTTACCCCTATTCCTCAATCTT 480
Db 471 TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTTCCCTCTTACCCCTATTCCTCAATCTT 530
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTCTTTACTCCCTCTCTCCC 540
Db 531 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTCTTTACTCCCTCTCTCCC 590
Qy 541 TTTTACCCCTCCATGTCGTTTAAAGGAGAGATGGGAGCATCTTCTGTTTATATCTCTGTA 600

Db	591	TTTTACCTCCATGGTCTGTTAAGGAGAGATGGGAGCATCATCTCTGTTATACCTCTGTA	650
Qy	601	CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTCCATAGTGGAGACTTGTCTTTTCAG	660
Db	651	CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTCCATAGTGGAGACTTGTCTTTTCAG	710
Qy	661	AACATAGGGATGAAGTAAAGTGCCTGAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT	720
Db	711	AACATAGGGATGAAGTAAAGTGCCTGAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT	770
Qy	721	AAGTTATTTTATATATATATATATAATAAATATATATAATACATATATAATATATATAG	780
Db	771	AAGTTATTTTATATATATATATATAATAAATATATATAATACATATATAATATATATAG	830
Qy	781	TGTGTGTGTATGCTGTGTGTAGACACACACGCATACACATATAATGGAAGCAATA	840
Db	831	TGTGTGTGTGTATGCTGTGTGTAGACACACACGCATACACATATAATGGAAGCAATA	890
Qy	841	AGCCATTTCTAAGAGCTTGTATGTTATGGAGGTCTGACTAGGCAATGATTTTCAGAGGCA	900
Db	891	AGCCATTTCTAAGAGCTTGTATGTTATGGAGGTCTGACTAGGCAATGATTTTCAGAGGCA	950
Qy	901	AGATTGGCATATCATTTCTAATAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	960
Db	951	AGATTGGCATATCATTTCTAATAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	1010
Qy	961	CTAAAAATAATAATAATAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	1020
Db	1011	CTAAAAATAATAATAATAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	1070
Qy	1021	CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGCTTCAGCAGTGTTCAGAGCCAAAGC	1080
Db	1071	CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGCTTCAGCAGTGTTCAGAGCCAAAGC	1130
Qy	1081	AAGAAGTTGAAGTGTGCTTACACAGAGGACATTAAGTATCATGCTCTCTTTAACTAGCAT	1140
Db	1131	AAGAAGTTGAAGTGTGCTTACACAGAGGACATTAAGTATCATGCTCTCTTTAACTAGCAT	1190
Qy	1141	CCCCGAAGTGGAGAAGGCTCAGCAGGCTCAAAAGGCATAGTCAATCCCAATCAGCCAACT	1200
Db	1191	CCCCGAAGTGGAGAAGGCTCAGCAGGCTCAAAAGGCATAGTCAATCCCAATCAGCCAACT	1250
Qy	1201	AAGTTGTCCTTTTCTGTTTCTGTTTCCATGGAACATTTGATTATAGTTAATCCTTC	1260
Db	1251	AAGTTGTCCTTTTCTGTTTCTGTTTCCATGGAACATTTGATTATAGTTAATCCTTC	1310
Qy	1261	TATCTTGAATCTT	1273
Db	1311	TATCTTGAATCTT	1323

RESULT 3
US-10-132-829-2
; Sequence 2, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
; FILE OF INVENTION: with vesicle vector
; FILE REFERENCE: 6627-Pal170
; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-132-829-2

Query Match	100.0%	Score 1273	DB 14	Length 2804
Best Local Similarity	100.0%	Pred. No. 1.5e-299		
Matches 1273	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	GGCCTCTCACTAACTAACTCACTTTCCCACTTTTGGTAGATTTTGAATATATACATTTCTAT	60	
Db	1464	GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTGGTAGATTTTGAATATATACATTTCTAT	1523	
Qy	61	GATCATTTGCTTTTCTCTTTTACAGGGGAGAAATTTCAATATTTTACCTTGAGCAAAATTTGATTA	120	
Db	1524	GATCATTTGCTTTTCTCTTTTACAGGGGAGAAATTTCAATATTTTACCTTGAGCAAAATTTGATTA	1583	
Qy	121	GAAATGGAACCACTAGAGGAATATATGTTGTTAGGAAATTTACAGTCATTTCTAAGGGCC	180	
Db	1584	GAAATGGAACCACTAGAGGAATATATGTTGTTAGGAAATTTACAGTCATTTCTAAGGGCC	1643	
Qy	181	CAGCCCTTGACAAAATTTGGAAGTTAAATTTCCCACTCTGTCCATCAGATACATATGGTTC	240	
Db	1644	CAGCCCTTGACAAAATTTGGAAGTTAAATTTCCCACTCTGTCCATCAGATACATATGGTTC	1703	
Qy	241	TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTTCCATCTTCCCGAT	300	
Db	1704	TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTTCCATCTTCCCGAT	1763	
Qy	301	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	360	
Db	1764	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	1823	
Qy	361	TTTGGTCTACTCTATCACAAGGCCAGTACCACTCATGAAAGAAAGAACACAGGAGTAGC	420	
Db	1824	TTTGGTCTACTCTATCACAAGGCCAGTACCACTCATGAAAGAAAGAACACAGGAGTAGC	1883	
Qy	421	TGAGAGGCTTAAACTCATCAAAAACACTACTCTCTTTTCTCTTCTTCTCTCTCTCTCTCC	480	
Db	1884	TGAGAGGCTTAAACTCATCAAAAACACTACTCTCTTTTCTCTTCTTCTCTCTCTCTCTCC	1943	
Qy	481	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC	540	
Db	1944	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC	2003	
Qy	541	TTTACCTTCCATGTCGTGTTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTCTGTA	600	
Db	2004	TTTACCTTCCATGTCGTGTTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTCTGTA	2063	
Qy	601	CACAGTTATACATGCTCATCAAAACCCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTCAG	660	
Db	2064	CACAGTTATACATGCTCATCAAAACCCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTCAG	2123	
Qy	661	AACATAGGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT	720	
Db	2124	AACATAGGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT	2183	
Qy	721	AAGTTATTTTATATATATATATATAATAAATATATATAATATATAATATAATATAATATAG	780	
Db	2184	AAGTTATTTTATATATATATATATAATAAATATATATAATATAATATAATATAATATAG	2243	
Qy	781	TGTGTGTGTATGGTGTGTGTAGACACACAGCATACACATATAATGGAAGCAATA	840	
Db	2244	TGTGTGTGTATGGTGTGTGTAGACACACAGCATACACATATAATGGAAGCAATA	2303	
Qy	841	AGCCATTTCTAAGAGCTTGTATGTTTATGGAGGTCTGACTAGGCAATGATTTTCAGAGGCA	900	
Db	2304	AGCCATTTCTAAGAGCTTGTATGTTTATGGAGGTCTGACTAGGCAATGATTTTCAGAGGCA	2363	
Qy	901	AGATTGGCATATCATTTGTAACATAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	960	
Db	2364	AGATTGGCATATCATTTGTAACATAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	2423	
Qy	961	CTAAAAATAATAATAATGCTTACAGAAAGAGAACCCGTTTGGTTCATCTACAG	1020	
Db	2424	CTAAAAATAATAATAATGCTTACAGAAAGAGAACCCGTTTGGTTCATCTACAG	2483	
Qy	1021	CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGCTTTTCAGCAGTGTTCAGAGCCNAGC	1080	

Db	2484	CTAGTAGAGACTTTGAGGAAGATTCAACAGTGTGCTTTCAGCAGGTTCAGAGCCAAGC	2543	
Qy	1081	AGAAAGTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTAACTAGCATA	1140	
Db	2544	AGAAAGTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTAACTAGCATA	2603	
Qy	1141	CCCCGAAGTGGAGAGGGTGACAGGCTCAAGGGCATTAAGTCATTTCCAATCAGCCAACT	1200	
Db	2604	CCCCGAAGTGGAGAGGGTGACAGGCTCAAGGGCATTAAGTCATTTCCAATCAGCCAACT	2663	
Qy	1201	AAGTTGCTCTTTTCTCGTTTCGGTTTCCCATGGAACATTTTGAATATATGTTAATCCTTC	1260	
Db	2664	AAGTTGCTCTTTTCTCGTTTCCCATGGAACATTTTGAATATATGTTAATCCTTC	2723	
Qy	1261	TATCTTGAATCTT	1273	
Db	2724	TATCTTGAATCTT	2736	
RESULT 4				
US-10-133-907-2				
; Sequence 2, Application US/10133907				
; Publication No. US20030195223A1				
; GENERAL INFORMATION:				
; APPLICANT: Chien, Kenneth R				
; APPLICANT: Hoshijima, Masahiko				
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII				
; TITLE OF INVENTION: with vesicle vector				
; FILE REFERENCE: 6627-PAL170				
; CURRENT APPLICATION NUMBER: US/10/133,907				
; CURRENT FILING DATE: 2002-04-25				
; PRIOR APPLICATION NUMBER: 60/286,314				
; PRIOR FILING DATE: 2001-04-25				
; NUMBER OF SEQ ID NOS: 5				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 2				
; LENGTH: 2804				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-133-907-2				
Query Match 100.0%; Score 1273; DB 16; Length 2804;				
Best Local Similarity 100.0%; Pred. No. 1.5e-299;				
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	GGCCTCTCACTAACTCACTTCCCATCTTTTGTAGATTGAAATATATACATTTCTAT	60	
Db	1464	GGCCTCTCACTAACTCACTTCCCATCTTTTGTAGATTGAAATATATACATTTCTAT	1523	
Qy	61	GATCATTGCTTTTCTTTACAGGGGAGNATTTTCATATTTTACCTGAGCNAATTTGATTA	120	
Db	1524	GATCATTGCTTTTCTTTACAGGGGAGNATTTTCATATTTTACCTGAGCNAATTTGATTA	1583	
Qy	121	GAAGATGGAAACCACTAGAGGAATATATGTTGTAGGAATTTACAGTCATTTCTAAGGGCC	180	
Db	1584	GAAGATGGAAACCACTAGAGGAATATATGTTGTAGGAATTTACAGTCATTTCTAAGGGCC	1643	
Qy	181	CAGCCCTTGACAAAATTTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTTC	240	
Db	1644	CAGCCCTTGACAAAATTTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTTC	1703	
Qy	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCATTTCCATCTTCCGAT	300	
Db	1704	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCATTTCCATCTTCCGAT	1763	
Qy	301	CTTCTTTGCTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	360	
Db	1764	CTTCTTTGCTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	1823	
Qy	361	TTTGGTCTACTCTATCACAGGCCAGTACACACTCATGAAAGAAACACAGGAGTAGC	420	
Db	1824	TTTGGTCTACTCTATCACAGGCCAGTACACACTCATGAAAGAAACACAGGAGTAGC	1883	

Qy	421	TGAGAGGCTAAACCTCATCAAAAAACACTACTCCTTTTCTCTACCCCTATTCTCTCAATCTT	480	
Db	1884	TGAGAGGCTAAACCTCATCAAAAAACACTACTCCTTTTCTCTACCCCTATTCTCTCAATCTT	1943	
Qy	481	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA	540	
Db	1944	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA	2003	
Qy	541	TTTTTACCCTCCATGCTGCTTAAAGGAGAGATGGGGAGCATCATTTCTGTATTACTTCTGTA	600	
Db	2004	TTTTTACCCTCCATGCTGCTTAAAGGAGAGATGGGGAGCATCATTTCTGTATTACTTCTGTA	2063	
Qy	601	CACAGTTATACATGCTATCAAAACCCAGACTTGTCTTCCATAGTGAGAGACTTGTCTTTTCA	660	
Db	2064	CACAGTTATACATGCTATCAAAACCCAGACTTGTCTTCCATAGTGAGAGACTTGTCTTTTCA	2123	
Qy	661	AACATAGGGATGAAGTAAGTGCTCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTT	720	
Db	2124	AACATAGGGATGAAGTAAGTGCTCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTT	2183	
Qy	721	AAGTTATTTTAG	780	
Db	2184	AAGTTATTTTAG	2243	
Qy	781	TGTGTGTGTATGCTGTGTAGACACACACGACATACACATATATATATATATATATATATAT	840	
Db	2244	TGTGTGTGTATGCTGTGTAGACACACACGACATACACATATATATATATATATATATATAT	2303	
Qy	841	AGCCATTCTAAGAGCTTGTATGGAGTCTGACTAGGCGATGATTTTTCACGAAGGCA	900	
Db	2304	AGCCATTCTAAGAGCTTGTATGGAGTCTGACTAGGCGATGATTTTTCACGAAGGCA	2363	
Qy	901	AGATTGGCATATCATTTGTAACCTAAAGAGCTGACATTTGACCCAGACATATTTGTACTCTT	960	
Db	2364	AGATTGGCATATCATTTGTAACCTAAAGAGCTGACATTTGACCCAGACATATTTGTACTCTT	2423	
Qy	961	CTAAAAATAATAATAATCTAACAAGAGAGAACCGTTTCGTTTGCATCTACAG	1020	
Db	2424	CTAAAAATAATAATAATCTAACAAGAGAGAACCGTTTCGTTTGCATCTACAG	2483	
Qy	1021	CTAGTAGAGACTTTGAGGAAGAAATTTCAACAGTGTCTTTCAGCAGTGTTCAGAGCCAAGC	1080	
Db	2484	CTAGTAGAGACTTTGAGGAAGAAATTTCAACAGTGTCTTTCAGCAGTGTTCAGAGCCAAGC	2543	
Qy	1081	AGAAAGTTGAAGTTGCTTAGACAGGACATTAAGTATCATGTCTCTTTTAACTAGCATA	1140	
Db	2544	AGAAAGTTGAAGTTGCTTAGACAGGACATTAAGTATCATGTCTCTCTTTTAACTAGCATA	2603	
Qy	1141	CCCCGAAGTGGAGAGGGTGACAGGCTCAAGGSCATAAGTCATTCCAAATCAGCCAAC	1200	
Db	2604	CCCCGAAGTGGAGAGGGTGACAGGCTCAAGGSCATAAGTCATTCCAAATCAGCCAAC	2663	
Qy	1201	AAGTTGTCTTTTCTGGTTTCTGTTTCCATGGAACATTTTGTATTAGTTAAATCCTTC	1260	
Db	2664	AAGTTGTCTTTTCTGGTTTCTGTTTCCATGGAACATTTTGTATTAGTTAAATCCTTC	2723	
Qy	1261	TATCTTGAATCTT	1273	
Db	2724	TATCTTGAATCTT	2736	

RESULT 5

US-10-956-157-357
; Sequence 357, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 357
; LENGTH: 2804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-357

Query Match 100.0%; Score 1273; DB 21; Length 2804;
Best Local Similarity 100.0%; Pred. No. 1.5e-299;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GGCCTCTCACTAATACTCTTCCCATCTTTTGGTAGATTTGAATATATACATCTAT 60
Db 1464 GGCCTCTCACTAATACTCTTCCCATCTTTTGGTAGATTTGAATATATACATCTAT 1523

Qy 61 GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAATTTGATTA 120
Db 1524 GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAATTTGATTA 1583

Qy 121 GAAAAATGGAAACCACTAGAGGAATATATATGTTAGGAAATTCACAGTCATTTCTAAGGGCC 180
Db 1584 GAAAAATGGAAACCACTAGAGGAATATATATGTTAGGAAATTCACAGTCATTTCTAAGGGCC 1643

Qy 181 CAGCCCTTGACAAAATTTGTAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC 240
Db 1644 CAGCCCTTGACAAAATTTGTAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC 1703

Qy 241 TCCACTATGGCACTAATCACTCACTCAATTTTCCCTCTTAGCAGCATTCATCTCCGAT 300
Db 1704 TCCACTATGGCACTAATCACTCACTCAATTTTCCCTCTTAGCAGCATTCATCTCCGAT 1763

Qy 301 CTCTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
Db 1764 CTCTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 1823

Qy 361 TTTGGTCTACTATATCAAGGGCCAGTACACACTCATGTAAGAAAGAACACAGGAGTAGC 420
Db 1824 TTTGGTCTACTATATCAAGGGCCAGTACACACTCATGTAAGAAAGAACACAGGAGTAGC 1883

Qy 421 TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTCTCTACCTCTACCTCTCAATCTT 480
Db 1884 TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTCTCTACCTCTACCTCTCAATCTT 1943

Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC 540
Db 1944 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC 2003

Qy 541 TTTTACCTCCATGGTCTGTTAAAGGAGAGATGGGAGCATCATTTCTGTTATACTTCTGTA 600
Db 2004 TTTTACCTCCATGGTCTGTTAAAGGAGAGATGGGAGCATCATTTCTGTTATACTTCTGTA 2063

Qy 601 CACAGTTATACATGTCTATCAAAACCCAGACTTGTCTCCATAGTGGAGACTGCTTTTCAG 660
Db 2064 CACAGTTATACATGTCTATCAAAACCCAGACTTGTCTCCATAGTGGAGACTGCTTTTCAG 2123

Qy 661 AACATAGGGATGAAGTAAAGTGGCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
Db 2124 AACATAGGGATGAAGTAAAGTGGCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 2183

Qy 721 AAGTTATTTTATATATATATATATATATATATATATATATATATATATATATATATATAG 780
Db 2184 AAGTTATTTTATATATATATATATATATATATATATATATATATATATATATATATATAG 2243

Qy 781 TGTGTGTGTATGCGTGTGTAGACACACACGACATACACATATAATATGGAAGCAATA 840
Db 2244 TGTGTGTGTATGCGTGTGTAGACACACACGACATACACATATAATATGGAAGCAATA 2303

Qy 841 AGCCATTTCTAAGAGCTTGTATGTTATGAGAGTCTGACTAGGAGATGATTTTCACGAGGCA 900
Db 2304 AGCCATTTCTAAGAGCTTGTATGTTATGAGAGTCTGACTAGGAGATGATTTTCACGAGGCA 2363
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RESULT 6

US-10-804-763-40
; Sequence 40, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 2804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-763-40

Query Match 100.0%; Score 1273; DB 21; Length 2804;
Best Local Similarity 100.0%; Pred. No. 1.5e-299;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GGCCTCTCACTAATACTCACTTTCCCATCTTTTGGTAGATTTGAATATATACATCTAT 60
Db 1464 GGCCTCTCACTAATACTCACTTTCCCATCTTTTGGTAGATTTGAATATATACATCTAT 1523

Qy 61 GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTTGATTA 120
Db 1524 GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTTGATTA 1583

Qy 121 GAAAAATGGAAACCACTAGAGGAATATATGTTAGGAAATTCACAGTCATTTCTAAGGGCC 180
Db 1584 GAAAAATGGAAACCACTAGAGGAATATATGTTAGGAAATTCACAGTCATTTCTAAGGGCC 1643

Qy 181 CAGCCCTTGACAAAATTTGTAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC 240
Db 1644 CAGCCCTTGACAAAATTTGTAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC 1703

Qy 241 TCCACTATGGCACTAATCACTCACTCAATTTTCCCTCTTAGCAGCATTCATCTCCGAT 300
Db 2724 TATCTTGAATCTT 2736
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Db 1704 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCAATTCATCTTCCCGAT 1763
Qy 301 CTTCTTTGCTTCTCCACCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
Db 1764 CTTCTTTGCTTCTCCACCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 1823
Qy 361 TTTGGTCTACTCTATCACAGGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420
Db 1824 TTTGGTCTACTCTATCACAGGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 1883
Qy 421 TGAGAGGCTAAACTCATCAAAACCACTACTCTCTTTTCCCTTACCCCTATTTCCTCAATCTT 480
Db 1884 TGAGAGGCTAAACTCATCAAAACCACTACTCTCTTTTCCCTTACCCCTATTTCCTCAATCTT 1943
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 540
Db 1944 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 2003
Qy 541 TTTTACCTCCCTCGTGTAAAGGAGAGATGGGAGCATCATTCGTGTTATATCTTCTGTGA 600
Db 2004 TTTTACCTCCCTCGTGTAAAGGAGAGATGGGAGCATCATTCGTGTTATATCTTCTGTGA 2063
Qy 601 CACAGTTATACATGTCCTATCAAAACCCAGACTTGCCTTCCATAGTGGAGACTTGCCTTTTCAG 660
Db 2064 CACAGTTATACATGTCCTATCAAAACCCAGACTTGCCTTCCATAGTGGAGACTTGCCTTTTCAG 2123
Qy 661 AACATAGGAGTGAAGTGAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
Db 2124 AACATAGGAGTGAAGTGAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 2183
Qy 721 AAGTTATTTATATATATATATATATAATAATATATAATATACAAATATAATATATAG 780
Db 2184 AAGTTATTTATATATATATATATATAATAATATATAATATACAAATATAATATATAG 2243
Qy 781 TGTGTGTGTATGCGTGTGTGTAGACACACACGACATACACATATAATGGAAGCAATA 840
Db 2244 TGTGTGTGTATGCGTGTGTGTAGACACACACGACATACACATATAATGGAAGCAATA 2303
Qy 841 AGCCATCTTAAGAGCTTGATGTTTATGAGGTCTGACTAGGATGATTTTCAGAAAGGCA 900
Db 2304 AGCCATCTTAAGAGCTTGATGTTTATGAGGTCTGACTAGGATGATTTTCAGAAAGGCA 2363
Qy 901 AGATTGGCATATCATTTGTAACATAAAAGCTGACATTTGACCCAGACATATTTGACTCTTT 960
Db 2364 AGATTGGCATATCATTTGTAACATAAAAGCTGACATTTGACCCAGACATATTTGACTCTTT 2423
Qy 961 CTAATAAATAATAATAATGCTTAACAGAAAGAGAACCGTTCCGTTTGCAATCTACAG 1020
Db 2424 CTAATAAATAATAATAATGCTTAACAGAAAGAGAACCGTTCCGTTTGCAATCTACAG 2483
Qy 1021 CTAGTAGAGACTTTGAGGAAGAAATCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAAGC 1080
Db 2484 CTAGTAGAGACTTTGAGGAAGAAATCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAAGC 2543
Qy 1081 AAGAAGTTGAAGTTGCTAGACCAGAGGACATAGTATCATGTCCTCTTTTAAGTACGATA 1140
Db 2544 AAGAAGTTGAAGTTGCTAGACCAGAGGACATAGTATCATGTCCTCTTTTAAGTACGATA 2603
Qy 1141 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAAAGGCATAAGTCATTTCCAATCAGCCAACT 1200
Db 2604 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAAAGGCATAAGTCATTTCCAATCAGCCAACT 2663
Qy 1201 AAGTTGTCCTTTTCTGGTTTCGTTTCACCATGGAAACATTTTGATTTATAGTTAATCCTTC 1260
Db 2664 AAGTTGTCCTTTTCTGGTTTCGTTTCACCATGGAAACATTTTGATTTATAGTTAATCCTTC 1260
Qy 1261 TATCTTGAATCTT 1273
Db 2724 TATCTTGAATCTT 2736

; Sequence 2125, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2125
; LENGTH: 38059
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 K02402
US-09-880-107-2125

Query Match 100.0%; Score 1273; DB 9; Length 38059;
Best Local Similarity 100.0%; Pred. No. 5.46-299;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCCTCTCACATACTAACTCACTTTCCCATCTTTTGTAGATTGAAATATATACATTTCTAT 60
Db 34393 GGCCTCTCACATACTAACTCACTTTCCCATCTTTTGTAGATTGAAATATATACATTTCTAT 34442
Qy 61 GATCATTTGCTTTTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTA 120
Db 34443 GATCATTTGCTTTTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTA 34502
Qy 121 GAAATGGAACCACTAGAGGAATATAATGTTAGGAAATTTACAGTCAATTTCTAGAGGCC 180
Db 34503 GAAATGGAACCACTAGAGGAATATAATGTTAGGAAATTTACAGTCAATTTCTAGAGGCC 34562
Qy 181 CAGCCCTTTGACAAAATTTGTAAGTTTAAATTTCTCCACTCTGTCACATCAGATCTATGTTTC 240
Db 34563 CAGCCCTTTGACAAAATTTGTAAGTTTAAATTTCTCCACTCTGTCACATCAGATCTATGTTTC 34622
Qy 241 TCCACTATGGCAACTTAACCTCACTCAATTTTCCCTCTTTAGCAGCAATTCATCTTCCCGAT 300
Db 34623 TCCACTATGGCAACTTAACCTCACTCAATTTTCCCTCTTTAGCAGCAATTCATCTTCCCGAT 34682
Qy 301 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
Db 34683 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 34742
Qy 361 TTTGGTCTACTCTATCACAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTAGC 420
Db 34743 TTTGGTCTACTCTATCACAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTAGC 34802
Qy 421 TGAGAGGCTAAACTCATCAAAACCACTACTCTCTTTTCCCTCTTACCCCTATTCCTCAATCTT 480
Db 34803 TGAGAGGCTAAACTCATCAAAACCACTACTCTCTTTTCCCTCTTACCCCTATTCCTCAATCTT 34862
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 540
Db 34863 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 34922
Qy 541 TTTTACCTCCCTCGTGTAAAGGAGAGATGGGAGCATCATTCGTGTTATATCTTCTGTGTA 600
Db 34923 TTTTACCTCCCTCGTGTAAAGGAGAGATGGGAGCATCATTCGTGTTATATCTTCTGTGTA 34982
Qy 601 CACAGTTATACATGTCCTATCAAAACCCAGACTTGCCTTCCATAGTGGAGACTTTCCTTTTCAG 660
Db 34983 CACAGTTATACATGTCCTATCAAAACCCAGACTTGCCTTCCATAGTGGAGACTTTCCTTTTCAG 35042

Qy	661	AACATAGGGATGAAGTGAAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTTCAGAGATT	720
Db	35043		
		AACATAGGGATGAAGTGAAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTTCAGAGATT	35102
Qy	721	AAGTTATTTTATATATATATATATATAATAATATATAATACAAATATAAATATATAG	780
Db	35103		
		AAGTTATTTTATATATATATATATATAATAATATATAATATAAATATATAG	35162
Qy	781	TGTTGTGTGTATGCGTGTGTGTAGACACACGCGATACACATATATATGGAAGCAATA	840
Db	35163		
		TGTTGTGTGTATGCGTGTGTGTAGACACACGCGATACACATATATGGAAGCAATA	35222
Qy	841	AGCCATCTTAAGAGCTTGATGCTTATGGAGGCTCTGACTAGGCATGATTTACGAAGGCA	900
Db	35223		
		AGCCATCTTAAGAGCTTGATGCTTATGGAGGCTCTGACTAGGCATGATTTACGAAGGCA	35282
Qy	901	AGATTGGCATATCATTTGTAACTAAAAAGCTGACATTGACCCAGACATATTTGACTCTTTT	960
Db	35283		
		AGATTGGCATATCATTTGTAACTAAAAAGCTGACATTGACCCAGACATATTTGACTCTTTT	35342
Qy	961	CTAAAAATAATAATAATGCTAAACAGAAAGAGAGAAACCGTTTCGTTTGCATCTACAG	1020
Db	35343		
		CTAAAAATAATAATAATGCTTAAACAGAAAGAGAGAAACCGTTTCGTTTGCATCTACAG	35402
Qy	1021	CTAGTAGAGACTTTTGAGGAAGAATTCAAACAGTGTGCTTTACACAGTGTTCAGAGCCAAAGC	1080
Db	35403		
		CTAGTAGAGACTTTTGAGGAAGAATTCAAACAGTGTGCTTTACACAGTGTTCAGAGCCAAAGC	35462
Qy	1081	AAGAAGTTGAAGTTGCCTAGACACAGAGGACATAAAGTATCATGTCTCTTTAACTAGCATATA	1140
Db	35463		
		AAGAAGTTGAAGTTGCCTAGACACAGAGGACATAAAGTATCATGTCTCTTTAACTAGCATATA	35522
Qy	1141	CCCCGAGTCGAGNAGGGTGCACAGGCTCAAAGGCATAAGTCATTTCCAATCAGCCAACT	1200
Db	35523		
		CCCCGAGTCGAGNAGGGTGCACAGGCTCAAAGGCATAAGTCATTTCCAATCAGCCAACT	35582
Qy	1201	AAGTTGTCTCTTTTCTCGTTTCTCGTTTCCACATGGAAACATTTTGGATTATAGTTAATCCCTTC	1260
Db	35583		
		AAGTTGTCTCTTTTCTCGTTTCTCGTTTCCACATGGAAACATTTTGGATTATAGTTAATCCCTTC	35642
Qy	1261	TATCTTGAATCTTT	1273
Db	35643		
		TATCTTGAATCTTT	35655

```

RESULT 8
US-09-118-748-1
: Sequence 1, Application US/09118748A
: Patent No. US20020031799A1
: GENERAL INFORMATION:
: APPLICANT: Stafford, Darrel W.
: APPLICANT: Chang, JinLi
: TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
: TITLE OF INVENTION: Activity
: FILE REFERENCE: 5470-183
: CURRENT APPLICATION NUMBER: US/09/118,748A
: CURRENT FILING DATE: 1998-07-17
: EARLIER APPLICATION NUMBER: 60/053,571
: EARLIER FILING DATE: 1997-07-21
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2792
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: sequence of
: OTHER INFORMATION: human factor IX-R338A
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (156)..(1400)
US-09-118-748-1

```

Query Match				99.7%;	Score 1269.8;	DB 9;	Length 2792;
Best Local Similarity				99.8%;	Pred. No. 9.3e-299;		
Matches 1271;				Conservative	0;	Mismatches	2;
						Indels	0;
						Gaps	0;
Qy	1	GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTGTAGATTTGAATATATACATTCCTAT	60				
Db	1452	GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTGTAGATTTGAATATATACATTCCTAT	1511				
Qy	61	GATCATTTGCTTTTCTCTTTTACAGGGGAGAAATTTTCATATTTTAACTCAGCAAAATGTAATTA	120				
Db	1512	GATCATTTGCTTTTCTCTTTTACAGGGGAGAAATTTTCATATTTTAACTCAGCAAAATGTAATTA	1571				
Qy	121	GAATAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATACAGTCATTTCTAAAGGCC	180				
Db	1572	GAATAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATACAGTCATTTCTAAAGGCC	1631				
Qy	181	CAGCCCTTGACAAATTTGCAAGTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC	240				
Db	1632	CAGCCCTTGACAAATTTGCAAGTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC	1691				
Qy	241	TCCACTATGGCAACTAACTCACATCAATTTTCCCTCTTAGCAGCATTTCCAATCTTCCCGAT	300				
Db	1692	TCCACTATGGCAACTAACTCACATCAATTTTCCCTCTTAGCAGCATTTCCAATCTTCCCGAT	1751				
Qy	301	CTTCTTTGCTTCTCCAAACCAAAACATCAATTTTATTTAGTTCTGTATACAGTACAGGATC	360				
Db	1752	CTTCTTTGCTTCTCCAAACCAAAACATCAATTTTATTTAGTTCTGTATACAGTACAGGATC	1811				
Qy	361	TTTGGTCTACTCTATCACAGGCCAGTACCACTCATGAAAGAAAGAACACAGGAGTAGC	420				
Db	1812	TTTGGTCTACTCTATCACAGGCCAGTACCACTCATGAAAGAAAGAACACAGGAGTAGC	1871				
Qy	421	TGAGAGCTAAAACTCATCAAAAACACTACTCTCTTTTCCCTACTACCTTATTCCTCAATCTT	480				
Db	1872	TGAGAGCTAAAACTCATCAAAAACACTACTCTCTTTTCCCTACTACCTTATTCCTCAATCTT	1931				
Qy	481	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT	540				
Db	1932	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT	1991				
Qy	541	TTTTACCTCCATGGTCTTTAAAGGAGAGATGGGAGCATCATTTCTGTATATCTTCTGTATA	600				
Db	1992	TTTTACCTCCATGGTCTTTAAAGGAGAGATGGGAGCATCATTTCTGTATATCTTCTGTATA	2051				
Qy	601	CACAGTTATACATGTCTATCAAAACCCAGACTCTCTTCCATAGTGGAGACTTGCTTTTTCAG	660				
Db	2052	CACAGTTATACATGTCTATCAAAACCCAGACTCTCTTCCATAGTGGAGACTTGCTTTTTCAG	2111				
Qy	661	AACATAGGGATGAAGTAAGTGCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATTT	720				
Db	2112	AACATAGGGATGAAGTAAGTGCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATTT	2171				
Qy	721	AAGTTATTTTATATATATAATATATATAAATATATAATATAACAATATAAATATATAG	780				
Db	2172	AAGTTATTTTATATATATAATATATATAAATATATAAATATAACAATATAAATATATAG	2231				
Qy	781	TGTGTGTGTCTATGCGTGTGTGTAGACACACACGTCATACACATATAATGGAAGCAATA	840				
Db	2232	TGTGTGTGTGTATGCGTGTGTGTAGACACACACGTCATACACATATAATGGAAGCAATA	2291				
Qy	841	AGCCATCTTAAAGACTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTTCAGAAAGGCA	900				
Db	2292	AGCCATCTTAAAGACTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTTCAGAAAGGCA	2351				
Qy	901	AGATTGGCATATCATTTGTAACATAAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT	960				
Db	2352	AGATTGGCATATCATTTGTAACATAAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT	2411				
Qy	961	CTAAAAATATAATAATAATGCTTAAACAGAAAGAGAGAACCGTTTCGTTTGCATCTACAG	1020				
Db	2412	CTAAAAATATAATAATAATGCTTAAACAGAAAGAGAGAACCGTTTCGTTTGCATCTACAG	2471				
Qy	1021	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTGTCTTTCCAGCAGTGTGTTTCAGAGCCAAAGC	1080				

Db	2472	CTAGTAGAGACTTTGAGGAGAAATTCACAGTGTGTCTTCAACAGTGTTCAGAGCCAAAGC	2531
QY	1081	AGAAGTTGAAGTTGGCTAGACAGAGGACATTAAGTATCATGTCTCTTTAACTAGCATA	1140
Db	2532	AAGAAGTTGAAGTTGGCTAGACAGAGGACATTAAGTATCATGTCTCTTTAACTAGCATA	2591
QY	1141	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAGGACATTAAGTATCATGTCTCTTTAACTAGCATA	1200
Db	2592	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAGGACATTAAGTATCATGTCTCTTTAACTAGCATA	2651
QY	1201	AAGTTGTCTCTTTCTCGTTTCTCGTTTCCACCATGGAACATTTTGAATATAGTTAACTCTTC	1260
Db	2652	AAGTTGTCTCTTTCTCGTTTCTCGTTTCCACCATGGAACATTTTGAATATAGTTAACTCTTC	2711
QY	1261	TATCTTGAATCTTT 1273	
Db	2712	TATCTTGAATCTTT 2724	
RESULT 9			
US-10-349-858-16			
; Sequence 16, Application US/10349858			
; Publication No. US20030220247A1			
; GENERAL INFORMATION:			
; APPLICANT: The Children's Hospital of Philadelphia			
; APPLICANT: HIGH, KATHERINE A.			
; APPLICANT: CAMIRE, RODNEY M.			
; APPLICANT: LARSON, PETER J.			
; APPLICANT: STAFFORD, DARREL W.			
; TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT C			
; FILE REFERENCE: 018743-0301425			
; CURRENT APPLICATION NUMBER: US/10/349,858			
; CURRENT FILING DATE: 2003-01-22			
; PRIOR APPLICATION NUMBER: 09/526,947			
; PRIOR FILING DATE: 2000-03-16			
; PRIOR APPLICATION NUMBER: 60/124,609			
; PRIOR FILING DATE: 1999-03-16			
; NUMBER OF SEQ ID NOS: 22			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 16			
; LENGTH: 2773			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-349-858-16			
Query Match 98.9%; Score 1259; DB 17; Length 2773;			
Best Local Similarity 99.8%; Pred. No. 4e-296;			
Matches 1271; Conservative 0; Mismatches 0; Indels 2; Gaps 1;			
QY	1	GGCCTCTCACTAACTAATCACTTCCCATCTTTTGTAGATTGGAATATATACATTTCTAT	60
Db	1435	GGCCTCTCACTAACTAATCACTTCCCATCTTTTGTAGATTGGAATATATACATTTCTAT	1494
QY	61	GATCATTTCTTTCTCTTACAGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA	120
Db	1495	GATCATTTCTTTCTCTTACAGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA	1554
QY	121	GAATAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTTCTAAGGGCC	180
Db	1555	GAATAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTTCTAAGGGCC	1614
QY	181	CAGCCCTTGACAAAATTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATCATATGGTTTC	240
Db	1615	CAGCCCTTGACAAAATTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATCATATGGTTTC	1674
QY	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTCTTAGCAGCATTTCCATCTTCCCGAT	300
Db	1675	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTCTTAGCAGCATTTCCATCTTCCCGAT	1734
QY	301	CTTCTTTTGTCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	360

Db	1735	CTTCTTTTGTCTTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	1794
QY	361	TTTGTGTCTACTCTATCAACAGCCAGTACCACTCATGTAAAGAAAGAAACACAGAGTAGC	420
Db	1795	TTTGTGTCTACTCTATCAACAGCCAGTACCACTCATGTAAAGAAAGAAACACAGAGTAGC	1854
QY	421	TGAGAGGGCTAAACCTCATCAAAACACACTACTCTCTTTCTCTACCCCTATTCCTCAATCTT	480
Db	1855	TGAGAGGGCTAAACCTCATCAAAACACACTACTCTCTTTCTCTACCCCTATTCCTCAATCTT	1914
QY	481	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA	540
Db	1915	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA	1974
QY	541	TTTTTACCTCCATGTCGTTAAAGAGAGATGGGGAGCATCATTCCTGTATTACTTCTGTA	600
Db	1975	TTTTTACCTCCATGTCGTTAAAGAGAGATGGGGAGCATCATTCCTGTATTACTTCTGTA	2034
QY	601	CACAGTTATACATGTCATCAAAACCCAGCTTGTCTTCCATAGTGAGACTTGTCTTTTTCAG	660
Db	2035	CACAGTTATACATGTCATCAAAACCCAGCTTGTCTTCCATAGTGAGACTTGTCTTTTTCAG	2094
QY	661	AACATAGGGATCAAGTAAAGTGCCTGAAAGTTTTGGGGGAAAAGTTTCTTTTCAGAGATT	720
Db	2095	AACATAGGGATCAAGTAAAGTGCCTGAAAGTTTTGGGGGAAAAGTTCCTTTTCAGAGATT	2154
QY	721	AAGTTATTTTATATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	780
Db	2155	AAGTTATTTTATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	2214
QY	781	TGTGTGTGTGTATGCTGT	840
Db	2215	TGTGTGTGTGTATGCTGT	2274
QY	841	AGCCATTCTAAGAGCTTCTGTATGGAGTCTGACTAGGCGATGATTTTCACGAAGGCA	900
Db	2275	AGCCATTCTAAGAGCTTCTGTATGGAGTCTGACTAGGCGATGATTTTCACGAAGGCA	2334
QY	901	AGATTGGCATATCATTTGTAATAAAGCTGACATTTGACCCAGACATATTGTACTCTTT	960
Db	2335	AGATTGGCATATCATTTGTAATAAAGCTGACATTTGACCCAGACATATTGTACTCTTT	2394
QY	961	CTAAAAATAATAATAATAATGCTTAACAGAAAGAGAGAACCGTTGTTGCAATCTACAG	1020
Db	2395	CT--AAATAATAATAATAATGCTTAACAGAAAGAGAGAACCGTTGTTGCAATCTACAG	2452
QY	1021	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAGC	1080
Db	2453	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAGC	2512
QY	1081	AAGAAAGTTGAAGTTGCGCTTAGACGAGGACATTAAGTATCATGTCTCTTTTAACTAGCATA	1140
Db	2513	AAGAAAGTTGAAGTTGCGCTTAGACGAGGACATTAAGTATCATGTCTCTTTTAACTAGCATA	2572
QY	1141	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAGGACATTAAGTATTCCTCAATCAGGCAACT	1200
Db	2573	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAGGACATTAAGTATTCCTCAATCAGGCAACT	2632
QY	1201	AAGTTGTCTCTTTTCTGGTTTCTGTTTCCATGGAACATTTTGTATTAGTTAACTCTTC	1260
Db	2633	AAGTTGTCTCTTTTCTGGTTTCTGTTTCCATGGAACATTTTGTATTAGTTAACTCTTC	2692
QY	1261	TATCTTGAATCTTT 1273	
Db	2693	TATCTTGAATCTTT 2705	

RESULT 10
US-10-741-600-3
; Sequence 3, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.

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; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2728)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-3

Query Match          98.9%; Score 1258.6; DB 21; Length 2728;
Best Local Similarity 99.8%; Pred. No. 4.9e-296;
Matches 1270; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 GGCCTCTCACTAACTCACTTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT 60
DB 1390 GGCCTCTCACTAACTCACTTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT 1449

QY 61 GATCATTTGCTTTTCTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATTGATTA 120
DB 1450 GATCATTTGCTTTTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATTGATTA 1509

QY 121 GAAATGGACCACTAGAGGAATATAATGTTAGGAAATACAGTCATTTCTTAAGGGCC 180
DB 1510 GAAATGGACCACTAGAGGAATATAATGTTAGGAAATACAGTCATTTCTTAAGGGCC 1569

QY 181 CAGCCCTTGACAAAATTTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 240
DB 1570 CAGCCCTTGACAAAATTTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 1629

QY 241 TCACATATGGCAACTAATCACTCAATTTTCCCTCTTACGAGCAATTTCCATCTTCCCGAT 300
DB 1630 TCACATATGGCAACTAATCACTCAATTTTCCCTCTTACGAGCAATTTCCATCTTCCCGAT 1689

QY 301 CTTCCTTTGCTTCTCCCAACCAACATCAATGTTTATAGTTCTGTATACAGTACAGATC 360
DB 1690 CTTCCTTTGCTTCTCCCAACCAACATCAATGTTTATAGTTCTGTATACAGTACAGATC 1749

QY 361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTAGC 420
DB 1750 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTAGC 1809

QY 421 TGAGAGGCTAAACTCATCAAAACACTACTCTCTTCTCTACCCCTATTCTCTCAATCTT 480
DB 1810 TGAGAGGCTAAACTCATCAAAACACTACTCTCTTCTCTACCCCTATTCTCTCAATCTT 1869

QY 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTTCTTCTTACTCCCTCTCTCC 540
DB 1870 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTTCTTCTTACTCCCTCTCTCC 1929

QY 541 TTTTACCCTCCATGGTCTGTTAAAGGAGAGATGGGAGAGCATCTTCTGTTATATCTTCTGTA 600
DB 1930 TTTTACCCTCCATGGTCTGTTAAAGGAGAGATGGGAGAGCATCTTCTGTTATATCTTCTGTA 1989

QY 601 CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTCAG 660
DB 1990 CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTTCCRTAGTGGAGACTTGTCTTTCAG 2049

QY 661 AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGATT 720
DB 2050 AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGATT 2109

QY 721 AAGTTATTTTATATATATATATATATAATAATAATATATATACAAATATAATATATAG 780
DB 2110 AAGTTATTTTATATATATATATATATAATAATAATATATATATAATAATAATATATA - 2168
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QY 781 TGTGTGTGTATGCTGTGTGTGTAGACACACACGCAATACACATATATAATGGAAGCAATA 840
DB 2169 -GTGTGTGTATGCTGTGTGTGTAGACACACACGCAATACACATATATAATGGAAGCAATA 2227

QY 841 AGCCATTCTTAAGAGCTTGTATGTTTATGAGGTCTGACTAGGCAATTTTCAGAAAGGCA 900
DB 2228 AGCCATTCTTAAGAGCTTGTATGTTTATGAGGTCTGACTAGGCAATTTTCAGAAAGGCA 2287

QY 901 AGATTGGCATATCATTTGTAACTAAAAAAGCTGACATTTGACCCAGACATATTTGTACTCTTT 960
DB 2288 AGATTGGCATATCATTTGTAACTAAAAAAGCTGACATTTGACCCAGACATATTTGTACTCTTT 2347

QY 961 CTAAAAATATAATAATAATAATGCTTAACAGAAAGAACCGTTCGTTTGAATCTACAG 1020
DB 2348 CTAAAAATATAATAATAATAATGCTTAACAGAAAGAACCGTTCGTTTGAATCTACAG 2407

QY 1021 CTAGTAGAGACTTTGAGGAGAAATTAACACAGTGTCTTTCAGCAGTGTTCAGAGCCNAGC 1080
DB 2408 CTAGTAGAGACTTTGAGGAGAAATTAACACAGTGTCTTTCAGCAGTGTTCAGAGCCNAGC 2467

QY 1081 AAGAAGTTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTAACTAGCATTA 1140
DB 2468 AAGAAGTTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTAACTAGCATTA 2527

QY 1141 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAAGGCATTAAGTCATTTCCAATCAGCCAAT 1200
DB 2528 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAAGGCATTAAGTCATTTCCAATCAGCCAAT 2587

QY 1201 AAGTTGCTCTTTTCTGTTTTCGTTTCCATGTCATGTTTGAATATAGTTTAACTCTTC 1260
DB 2588 AAGTTGCTCTTTTCTGTTTTCGTTTCCATGTCATGTTTGAATATAGTTTAACTCTTC 2647

QY 1261 TATCTTGAATCTT 1273
DB 2648 TATCTTGAATCTT 2660

RESULT 11
US-10-741-600-1
; Sequence 1, Application US/10741.600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2771
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2771)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-741-600-1

Query Match          98.9%; Score 1258.6; DB 21; Length 2771;
Best Local Similarity 99.8%; Pred. No. 5e-296;
Matches 1270; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 GGCCTCTCACTAACTCACTTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT 60
DB 1433 GGCCTCTCACTAACTCACTTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT 1492

QY 61 GATCATTTGCTTTTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATTGATTA 120
DB 1493 GATCATTTGCTTTTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATTGATTA 1552

QY 121 GAAATGGAAACCACTAGAGGAATATAATGTTTAGGAAATACAGTCATTTCTTAAGGGCC 180
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Db 1553 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAATATACAGTCAATTTCTAAGGGCC 1612
Qy 181 CAGCCCTTGACAAAATGTGAAGTTAAATCTCCACTCTGTCCATCAGATACATATGTTTC 240
Db 1613 CAGCCCTTGACAAAATGTGAAGTTAAATCTCCACTCTGTCCATCAGATACATATGTTTC 1672
Qy 241 TCCACTATGCGCACTAACTCACTCAATTTTCCCTCTTAGCAGCAATTCCTCCGAT 300
Db 1673 TCCACTATGCGCACTAACTCACTCAATTTTCCCTCTTAGCAGCAATTCCTCCGAT 1732
Qy 301 CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCGTATACAGTACAGGATC 360
Db 1733 CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCGTATACAGTACAGGATC 1792
Qy 361 TTTGCTCTACTCTATCACAAGGCGAGTACACACTCATGAAGAAAGAAACACAGGAGTAGC 420
Db 1793 TTTGCTCTACTCTATCACAAGGCGAGTACACACTCATGAAGAAAGAAACACAGGAGTAGC 1852
Qy 421 TGAGAGGCTAAACTCATCAAAACACACTACTCCTTTTCCCTCTACCTATTCTCAATCTT 480
Db 1853 TGAGAGGCTAAACTCATCAAAACACACTACTCCTTTTCCCTCTACCTATTCTCAATCTT 1912
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTTCTTTTCTTTTCTCTCTCC 540
Db 1913 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTTCTTTTCTTTTCTCTCC 1972
Qy 541 TTTTACCCTCCATGTCGTGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTGTGA 600
Db 1973 TTTTACCCTCCATGTCGTGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTGTGA 2032
Qy 601 CACAGTTATACATGCTATCAAAACCCAGACTTGTCTTCCATAGTGGAGCTCTCTTTTCAG 660
Db 2033 CACAGTTATACATGCTATCAAAACCCAGACTTGTCTTCCRTAGTGGAGACTTGTCTTTTCAG 2092
Qy 661 AACATAGGGATGAAGTGAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
Db 2093 AACATAGGGATGAAGTGAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 2152
Qy 721 AAGTTATTTTATATATATATATATATAATAATATATAATAATATATAATAATATATAG 780
Db 2153 AAGTTATTTTATATATATATATATAATAATATATAATAATATATAATAATATATA- 2211
Qy 781 TGTGTGTGTATGCTGT 840
Db 2212 -GTGTGTGTGTATGCTGT 2270
Qy 841 AGCCATTTCTAAGAGCTTGTATGTTATGAGGCTGTGACTAGGATGATTTTCAAGAGCA 900
Db 2271 AGCCATTTCTAAGAGCTTGTATGTTATGAGGCTGTGACTAGGATGATTTTCAAGAGCA 2330
Qy 901 AGATTGGCATATCATTTGTAATCAAAAAGCTGACATTTGACCCAGACATATGTTCTTTT 960
Db 2331 AGATTGGCATATCATTTGTAATCAAAAAGCTGACATTTGACCCAGACATATGTTCTTTT 2390
Qy 961 CTAAAAATAATATAATATGCTATCAGAAAGAGAGACCGTTCGTTTGCATCTACAG 1020
Db 2391 CTAAAAATAATATAATATGCTATCAGAAAGAGAGACCGTTCGTTTGCATCTACAG 2450
Qy 1021 CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAGC 1080
Db 2451 CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAGC 2510
Qy 1081 AAGAAGTTGAAGTTGCTTAGACAGAGGACATAAGTATCATGTCTCTTTTAACTAGCATTA 1140
Db 2511 AAGAAGTTGAAGTTGCTTAGACAGAGGACATAAGTATCATGTCTCTTTTAACTAGCATTA 2570
Qy 1141 CCCCAGAGTGGAGAGGGTGCAGAGGCTCAAGGCATTAAGTCAATTCAGCCACT 1200
Db 2571 CCCCAGAGTGGAGAGGGTGCAGAGGCTCAAGGCATTAAGTCAATTCAGCCACT 2630
Qy 1201 AAGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGAATATATAGTTTAACTCTTC 1260

Db 2631 AAGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGAATATATAGTTAATCCTTC 2690
Qy 1261 TATCTTGAATCTT 1273
Db 2691 TATCTTGAATCTT 2703
RESULT 12
US-10-741-600-2
; Sequence 2, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73957
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2777)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-2
Query Match 98.9%; Score 1258.6; DB 21; Length 2777;
Best Local Similarity 99.8%; Pred. No. Se-296;
Matches 1270; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
Qy 1 GGCCTCTCACAACTAACTCACTTTCCCATCTTTGTTAGATTGAAATATATACATTTCTAT 60
Db 1439 GGCCTCTCACAACTAACTCACTTTCCCATCTTTGTTAGATTGAAATATATACATTTCTAT 1498
Qy 61 GATCATTTCTTTTCTTTTACAGGGGAGAAATTTTCAATATTTTACCTGAGCAAAATGATTA 120
Db 1499 GATCATTTCTTTTCTTTTACAGGGGAGAAATTTTCAATATTTTACCTGAGCAAAATGATTA 1558
Qy 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAATATACAGTCAATTTCTAAGGGCC 180
Db 1559 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAATATACAGTCAATTTCTAAGGGCC 1618
Qy 181 CAGCCCTTGACAAAATTTGAAAGTTAAATTTCTCCACTCTGCCATCAGATACATATGTTTC 240
Db 1619 CAGCCCTTGACAAAATTTGAAAGTTAAATTTCTCCACTCTGCCATCAGATACATATGTTTC 1678
Qy 241 TCCACTATGCGCACTAACTCACTCAATTTTCCCTCTTAGCAGCAATTCATCTTCCGAT 300
Db 1679 TCCACTATGCGCACTAACTCACTCAATTTTCCCTCTTAGCAGCAATTCATCTTCCGAT 1738
Qy 301 CTTCTTTCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCGTATACAGTACAGGATC 360
Db 1739 CTTCTTTCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCGTATACAGTACAGGATC 1798
Qy 361 TTTGCTCTACTCTATCACAAGGCGAGTACACACTCATGAAGAAAGAAACACAGGAGTAGC 420
Db 1799 TTTGCTCTACTCTATCACAAGGCGAGTACACACTCATGAAGAAAGAAACACAGGAGTAGC 1858
Qy 421 TGAGAGGCTAAACTCATCAAAAAACATCACTCTTTTCCCTCTACCTATTCTCAATCTT 480
Db 1859 TGAGAGGCTAAACTCATCAAAAAACATCACTCTTTTCCCTCTACCTATTCTCAATCTT 1918
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTTCTTTTCTCTCTCTCTCC 540
Db 1919 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTTCTTTTCTCTCTCTCTCC 1978
Qy 541 TTTTACCCTCCATGTCGTGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTGTGA 600
Db 1979 TTTTACCCTCCATGTCGTGTTAAAGGAGAGATGGGAGCATCATCTGTTTATCTGTGA 2038

[illegible]

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RESULT 14
US-10-741-600-17553
; Sequence 17553, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17553
; LENGTH: 44752
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(44752)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Table
US-10-741-600-17553

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Db	3775	TTTGGTCTACTCTATCACAAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC	37834
Qy	421	TGAGAGCTAAAACCTCATCAAAAAACACTACTCTCTTTTCTCTFACCCCTATTTCTCTCAATCTT	480
Db	37835	TGAGAGCTAAAACCTCATCAAAAAACACTACTCTTTTCTCTFACCCCTATTTCTCTCAATCTT	37894
Qy	481	TTACCTTTTCCAAATCCCAATCCCAAAATCAGTTTTTCTTTCTTTTACTCCCTCTCTCCC	540
Db	37895	TTACCTTTTCCAAATCCCAATCCCAAAATCAGTTTTTCTTTCTTTTACTCCCTCTCTCCC	37954
Qy	541	TTTTTACCTCCATGGTGGTTAAAGGAGAGATGGGAGCATCATTTCTGTGTATCTTCTGTATA	600
Db	37955	TTTTTACCTCCATGGTGGTTAAAGGAGAGATGGGAGCATCATTTCTGTGTATCTTCTGTATA	38014
Qy	601	CACAGTTATACATGTCATCAAAACCAGACTTGTCTTCATATGAGAGACTTGTCTTTTCAG	660
Db	38015	CACAGTTATACATGTCATCAAAACCAGACTTGTCTTCATATGAGAGACTTGTCTTTTCAG	38074
Qy	661	AACATAGGATGAAGTGAAGTGCCCTGAAAGTTTGGGGGAAAGTTTCTTTTCAGAGAGTT	720
Db	38075	AACATAGGATGAAGTGAAGTGCCCTGAAAGTTTGGGGGAAAGTTTCTTTTCAGAGAGTT	38134
Qy	721	AAGTTATTTATATATATATATATATATAATAATATATAATAATAATAATAATAATAATA	780
Db	38135	AAGTTATTTATATATATATATATATATAATAATAATAATAATAATAATAATAATAATA	38193
Qy	781	TGTGTGTGTATGCGTGTGTGTAGACACACACGATACACACATATAATGGAAGCAATA	840
Db	38194	-GTGTGTGTGTATGCGTGTGTGTAGACACACACGATACACACATATAATGGAAGCAATA	38252
Qy	841	AGCCATCTTAAGAGCTTGATGGTTATGGAGTCTGACTAGGCGATGATTTTCAAGAAAGCA	900
Db	38253	AGCCATCTTAAGAGCTTGATGGTTATGGAGTCTGACTAGGCGATGATTTTCAAGAAAGCA	38312
Qy	901	AGATTGGCATATCAATTGTGTAATAAAAGCTGACATTTGACCCAGACATATTGTACTCTTT	960
Db	38313	AGATTGGCATATCAATTGTGTAATAAAAGCTGACATTTGACCCAGACATATTGTACTCTTT	38372
Qy	961	CTAAAATAATATAATAATGCTTAACAGAAAGAGAACCGTTTCGTTTGGAAATCTACAG	1020
Db	38373	CTAAAATAATATAATAATGCTTAACAGAAAGAGAACCGTTTCGTTTGGAAATCTACAG	38432
Qy	1021	CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTCTTTTCAGCAGTGTTCAGAGCCAAAGC	1080
Db	38433	CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTCTTTTCAGCAGTGTTCAGAGCCAAAGC	38492
Qy	1081	AAGAAGTTGAAGTTGCCTAGACACAGAGGACATAAGATATCATGTCTCTTTTAACTAGCATATA	1140
Db	38493	AAGAAGTTGAAGTTGCCTAGACACAGAGGACATAAGATATCATGTCTCTTTTAACTAGCATATA	38552
Qy	1141	CCCCGAAGTGGAGAGGGTGCAGAGGCTCAAGAGGCATAAGTTCATCCCAATCAGGCCAACT	1200
Db	38553	CCCCGAAGTGGAGAGGGTGCAGAGGCTCAAGAGGCATAAGTTCATCCCAATCAGGCCAACT	38612
Qy	1201	AAGTTGTCTCTTTTCTGGTTTCGTGTTTCCACATGGAAACATTTTGTATTAGTAAATCCTTC	1260
Db	38613	AAGTTGTCTCTTTTCTGGTTTCGTGTTTCCACATGGAAACATTTTGTATTAGTAAATCCTTC	38672
Qy	1261	TATCTTGAATCTTT 1273	
Db	38673	TATCTTGAATCTTT 38685	

RESULT 15
US-09-864-761-13921
SEQUENCE 13921, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED

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Query Match	69.4%	Score 883.4	DB 9	Length 1971
Best Local Similarity	99.7%	Pred. No. 1.2e-204		
Matches 896	Conservative 0	Mismatches 1	Indels 2	Gaps 1
Qy	1	GGCCTCTCACTAACTAACTCACTCTTCCCATCTTTTGGATATTTGAATATATACACTTCAT	60	
Db	1075	GGCCTCTCACTAACTAACTCACTTCCCATCTTTGTTAGATTTGAATATATACACTTCAT	1134	
Qy	61	GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTGATTA	120	
Db	1135	GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTGATTA	1194	
Qy	121	GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTCACAGTCATTTCTTAAGGGCC	180	
Db	1195	GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTCACAGTCATTTCTTAAGGGCC	1354	
Qy	181	CAGCCCTTGACAAAATTTGTAAGHTAAATTTCTCCACCTCTGTCATCAGATACATATGGTTC	240	
Db	1255	CAGCCCTTGACAAAATTTGTAAGHTAAATTTCTCCACCTCTGTCATCAGATACATATGGTTC	1314	
Qy	241	TCCACTATGGCAACTAACTCACTCAATTTTTTCCCTCCTTTAGCAGCATTTCCATCTTCCCGAT	300	

Search completed: October 4, 2005, 18:26:23
Job time : 882 secs

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